

FIGURE 1

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGGCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCTGAGGCCCCCAGC
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCCTGGGC
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGGAGGCACAGGTGGCCCCCACCACCCGGAGG
AGCAGTCTCTGCCCCCTGTCCGGGGGATGACTGATTCTCTCTCCGCCAGGCCACCCAGAGGAGA
AGGCCACCCCGCCTGGAGGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGTGATGTGGCT
TCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTTAGGGTGTGTGCT
GTCCCGGGCTCACGGGACCCCTGTCTCCGAGTCGTTCTGTGCAGCGTGTGTACCGACCCCTTC
TCACCACCTGCGACGGGCACCGGCCCTGCAGCACCTACCGAACCATTTATAGGACCGCCTAC
CGCCCGAGCCCTGGGCTGGCCCTTGCACGGCCTCGCTACGCGTGTGCCCCGGCTGGAAGAG
GACCAGCGGCTTCTCTGGGGCTGTGGAGCAGCAATATGCCAGCGCCATGCCGGAACGGAG
GGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCAG
TCAGATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGC
CGGCAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTG
TGCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCATGAAG
GAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCT
GGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCC
TCCTGGTGCACCTCCTTCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTTC
CTGGAGGAGCAGCTGGGGTCTGTCTCTGCAAGAAAGACTCGTGA~~CT~~GTGCCAGCGCCCCAGG
CTGGACTGAGCCCCCTCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGTCT
CAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCTCTCTTTCTCTCTC
CCCTTCCCTCGGGAGGGTCCCCAGACCTTGGCATGGGATGGGCTGGGATTTTTTTTGTGAAT
CCACCCCTGGCTACCCCCACCTTGGTTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCA
CTGAGGGAAGGTACGAGTTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCC
CGGAGGCTGGGTGGGGCTCAGTGGGGCTGCTGCCTGACCCCGAGCACAATAAAAAATGAAA
CGTGAAGGGCGGCCGCGACTCT
AGAGTCGACCTGCAGAAGCTTGGCCGCATGGCCCAACTTGTTATTGCGACTTATAATGGT
TACAAAT

FIGURE 2

MTDSPPPGHPEEKATPPGGTGHEGLSGGAADVASGVSGRHRARLPARPLGCVLSRAHGDPV
SESFVQRVYQFFLITCDGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGAC
GAAICQPPPCRNGGSCVQPGRCRCPCAGWRGDTQCQSDVDECSARRGGCPQRCINTAGSYWCQCW
EGHSLSADGTLCVPKGGPPRVAPNPPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLAS
QALEHGLPDPGSLLVHSFQQLGRIDSLSEQISFLEEQLGSCSCCKDS

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 93-97, 270-274

N-myristoylation sites.

amino acids 19-25, 78-84, 97-103, 100-106, 103-109, 157-163,
191-197, 265-271

Amidation site.

amino acids 26-30

Aspartic acid and asparagine hydroxylation site.

amino acids 152-164

Cell attachment sequence.

amino acids 130-133

EGF-like domain cysteine pattern signature.

amino acids 123-135

FIGURE 3

CGCTCGCCCCGTGCGCCCTCGCCTCCCCGCAGAGTCCCTCGCGGCAGCAGATGTGTGTGGG
 GTCAGCCACCGGCGGGGACTATGGTGAAATTCCTCGGCGCTCAGCAGCTACTGGCCCCGTGATC
 CGCTTTCTTGGTGCCCTGTGGGCATCAACACATAGCCATCGACTTCGGGGAGCAGGCCCTTGAA
 CCGGGGCGATTGTCTGTGTCAAGGAGGATGCAGTGCAGATGCTGGCCAGCTACCGGGCTGGCGT
 ACTCCCTCATGAAGTTCTTTCACGGGTCCCATGAGTGACTTCAAAATGTGGGCTGGTGT
 GTGAACAGCAAGAGAGACAGGACCAAGCCGTCTGTGTATGTGTGGTGGCAGGGGCCATCGC
 TGCCGTCTTTACACACTGATAGCTTATAGTGATTAGGATACACTATTCAATAAACTGC
 ACCATGTGGACGAGTTCGGTGGGGAGCAAGACGAGAAGGGCTTCCTGTACTCTCGCCGCTTT
 CCTTTTCATGACGCAATGGCATGGACCCATGCTGGCATTCTCTTAAACACAAATACAGTTT
 CCTGGTGGGATGTGCCTCAATCTCAGATGTCATAGCTCAGGTTGTTTTGTAGCCATTTTGC
 TTACAGTCACTCGGAATGCCGGAGCCCTGCTCATCCCGATCCTCTCCTTGATACATGGGC
 GCACTTGTGCGCTGCACCACCTGTGCTGGGCTACTACAAGAACATTACAGACATCATCCC
 TGACAGAAGTGGCCCGGAGCTGGGGGAGATGCAACAATAAGAAAGATGCTGAGCTTCTGGT
 GGCCTTTGGCTCTAATTCTGGCCACACAGAGAATTCAGTTCGGGCTATTGTCAACCTCTTTGTT
 TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGGATTTTGACAGCCACATA
 CCTGTGGGTACATGCCATACGGCTGGTTGACGGAATCCGTGCTGTGTACTCTGCTTTTCG
 ACAAGAATAACCCAGCAACAACTGGTGAGCACGAGCAACACAGTACGGCAGCCCCACATC
 AAGAAGTTCACTTCTGCTGTCATGGCTCTGTCACTCAGCTCTGTTTCGTGATGTTTTGGAC
 ACCCAACGTGTCTGAGAAAACTTGATAGACATCATCGGAGTGGAATTTGCCCTTTCAGAAC
 TCTGTGTGTTTCTTTGCGGATCTTCTCCTTCTTCCAGGTTCCAGTCACAGTGAAGGGCGCAT
 CTCACGGGTGGCTGATGACACTGAAGAAAACCTTCGTCCTGCCCCAGCTCTGTGCTGCG
 GATCATCGTCTCATCGCCAGCTCGTGGTCTTACCCTAAGTGGGGGTGCACGGTCCGACCC
 TGGGCGTGGGCTCCCTCTGGCGGGCTTTGTGGGAGAATCCACCATGGTGCCTCATCGCTGCG
 TGCTATGTTTACCGGAGACGAAAAAGAAGATGGAGAATGAGTCGGCCACGAGGGGGGAAGA
 CTCTGCCATGACAGACATGCCTCCGACAGAGGAGGTGACAGACATCGTGGAAATGAGAGAGG
 AGAATGAATTAAGCACGGGACGCCATGGGCAGTGCAGGGACGGTCAGTCAGGATGACACTTC
 GGCATCATCTCTTCCCTCTCCCATCGTATTTTGTTCCTTTTTTGTGTTTTGGTAAAT
 GAAAGAGGCCCTGATTTAAAGGTTTCGTGTCAATTCTCTAGCATACTGGGTATGCTCACACT
 GCGTGGGGGACTAGTGAATGGTCTTACTGTTGCTATGTAATAACAAACGAAACAACTGAC
 TTCATACCCCTGCCTCACGAAACCCAAAGACACAGCTGCCTCAGGGTTGACGTTGTGTCT
 TCCTCCCTGGACAATCTCCTCTTGGAACCAAAGGACTGCAGCTGTGCCATCGCGCTCGGT
 CACCCTGCACAGCGGCCACAGACTCTCCTGTCCCTTTCATCGCTCTTAAGAATCAACAGG
 TTAATACTCGGCTTCTTTGATTGCTTCCAGTCACATGGCCGTACAAGAGATGGAGCCC
 CGGTGGCTCTTAATTTCCCTTCTGCCACGGAGTTCGAACCATCTACTCCACACATGCAG
 GAGGCGGGTGGCACGCTGCAGCCCGAGTCCCGTTTACACTGAGGAACGGAGACCTGTGAC
 CACAGCAGGCTGACAGATGGACAGAATCTCCCGTAGAAAGGTTTGGTTTGAAGTCCCCGGG
 GGCACAAACTGACATGGTTGAATGATAGCACTTCACTCTGCGTTCTCTGATCTGAGCAA
 GCTGTGAGTCTCACCACCACCGTGTATATACATGAGCTAACTTTTTTAAATGTCAAAAA
 GCGCATCTCCAGATTCCAGACCTGCGCGCATGACTTTTCTGAAAGGCTTGCTTTTCCCTCGC
 CTTTCTGAGGTCGATTAGAGCGAGTACATGAGGACATCTAACTTTGCAATTTTGTATTT
 TACAGTGAATCGAAGCTTTAAGTCTCATCCAGCATCTAATGCCAGGTTGCTGTAGGGTAAC
 TTTTGAAGTATATATTACCTGTTCTGCTATCCTTAGTCATAACTCTGCGGTACAGGTAA
 TTGAGAATGTACTACGGTACTTCCCTCCACACCATACGATAAAGCAAGACATTTTATAACG
 ATACAGAGTGCATATGTGGTCTCCCTGAAATAACGCATTTCGAAATCCATGCAGTGCAGTA
 TATTTTTCTAAGTTTTGGAAGCAGGTTTTTTCTTTAAAAAATATAGACACGGTTCACT
 AAATTGATTAGTCAGAAATCTTAGACTGAAAGAACCTAAACAAAAAATATTTTAAAGATA
 TAAATATATGCTGTATATGTTATGTAATTTATTTAGGCTATAATACATTTCTCTATTTTCG
 ATTTTCAATAAAATGCTCTAATACAAAAA

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FIGURE 4

MVKFPALTHYWPLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMKFF
TGPMSEDFKNVGLVFNISKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYIIINKLHHVDESV
GSKTRRAFLYLAAFFPMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFVAILLHSHLEC
REPLILPILSLYMGALVRCCTTLCIGYYKNIHDIIPDRSGPELGGDATIRKMLSPWWPLALIL
ATQIRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMPYGWLTEIRAVYPAFDKNNPSN
KLVSTSNVTAAHIKKFTFVCMALSLTLCFVMFWTPNVSEKILIDIIGVDFAFaelcVvPLR
IFSFFPVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYLGvHGATLGvGSLL
AGFVGESTMVAIAACYVYRKQKKMENESATEGEDSAMTDMPTEEVTDIVEMREENE

Transmembrane domains:

amino acids 86-106, 163-179, 191-205, 237-253, 327-343, 357-374,
408-423, 431-445

FIGURE 5

CCTGACAGAAGTGCCCCGGAGCTGGGGGAGATNCAACATTAAGAAGATGCTGAGCTTCTGGT
GCCNTTTGGCTCTAATTCTGGCCACACAGAGAANCAGTCGGCCTATTGTCAACCTCTTTGTT
TCCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA
CCCTGTGGGTACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTCG
ACAAGAATAACCCAGCAACAACTGGTGAGCACGAGCAACACAGTCACGGCGGCCACATC
AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTTGGAC
ACCCAACGTGTCTGNAAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTGCAGAAC
TCTGTGTTGTTCCCTTTGCGGATCTTCTCCTTCTTCCAGTCCAGTCACAGTGAGGGCGCAT
CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGTC

FIGURE 6

TGACGGAATCCCGGGCTGGGTATCCTGGTTTNGACAAGATAAAACCCCGAGCAANAAATTGGG
GAGCAGGGCAAACAGTNACGGGCAGCCACATCAAGAAGTTCACCTTNGTTTGNATGGNTC
TGTCAACTCACGCTNTGTTTCGTGATGTTTTGGACACCCAAAGTGTTTGAGAAAAATTTGAT
AGACATNATCGGAGTGGANTTTGCCCTTTCAGAAANTTGNNGNTGTTCCCTTTCGGGATTTTCT
CCTTTTTCCAGTTCAGTCACAGNAGGGCGCATCTACCGGGNGGNTGATGACANTGAAG
AAAACCTTTGTCTTGCCCCAGCTNTTTGGTGCGGATCATTGTCCTNATNGCCAGCCTTGT
GGTCCTACCCCTACCTGGGGGTGCACGGTGCGACCTGGGCGTGGGTTCCCTCCTGGCGGGCA

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FIGURE 7

TATTCACAGTTCGGTCACGGGGAGGGCGCATNTACCGGGTGGCTGANGAACTGAAGAAA
ACCTTNGTCCTTGCCCCAGNTTTGTGNTGCGGATNATCGTCCTCATCGCCAGCCTNGTGGT
CCTACCTACCTGGGGGTGCACGGTGAGAC

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FIGURE 8

CCCCCGCGCCCGGCGCGGGCGCCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGA
GCCTGCTCCCCTGCTCAGCTGCGCGTCTTGCTCTGCGGCTCTGCCCTGTCATCTGTGCAG
CTGCTGCCCCGCCAGCCGCAACTCCACCGTGAGCCGCTCATCTTCAAGTTCTTCTCTTCC
TGGGGGTGCTGGTGTCCATCATTTATGCTGAGCCCGGGCGTGGAGAGTCAGCTCTACAAGCTG
CCCTGGGTGTGTGAGGAGGGGGCCGGATCCCCACCGTCTGTCAGGGCCACATCGACTGTGG
CTCCCTGCTTGGGTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGCCTTCTTCTTCT
TCTTTTTCACCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCGGCTGCCATCCAG
AATGGGTTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCCTACCGTGGGTGCCTTCTACAT
CCCTGACGGCTCCTTCACCAACATCTGGTTCTACTTCGGCGTCTGGGCTCCTTCTCTTCA
TCCTCATCCAGCTGGTGTGCTCATCGACTTTGCGCACTCCTGGAACCAGCGGTGGCTGGGC
AAGGCCGAGGAGTGCGAATTCGGTGCTGTGATGTTTCATGTACTACACTGAGCCGACGGCT
CTACTTGCTGTGATGCTGCGGCGGTGGCGCTGATGTTTCATGTACTACACTGAGCCGACGGCT
GCCACGAGGGCAAGTCTTCATCAGCCTCAACCTCACCTTCTGTGCTGCGGTGTCATCGCT
GCTGTCTGCCCCAAGGTCCAGGACGCCAGCCCAACTCGGGTCTGTGTCAGGCTCGGTCTCAT
CACCTCTACACCATGTTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCA
ACCCCATTTTGCCAAACCCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAG
ACCCAGTGGTGGGATGCCCGAGCATTGTGGGCCTCATCATCTTCTCTGTGACCCCTCTT
CATCAGTCTGCGCTCCTCAGACCACCGGCAGGTGAACAGCCTGATGTCAGACCGAGGAGTGCC
CACCTATGCTAGACGCCACACAGCAGCAGCAGCAGCAGGTGGCAGCTGTGAGGGCCGGGCC
TTTGACAACGAGCAGGACGGCGCTACCTACAGCTACTCCTTCTTCCACTTCTGCTGCTGTGCT
GGCCTCACTGCACGTCTATGATGACGCTCACCAACTGGTACAAGCCCGGTGAGACCCGAAGA
TGATCAGCACGTGGACCGCGGTGTGGGTGAAGATCTGTGCCAGCTGGGCGAGGCTGCTCCTC
TACCTGTGAGACCTGGTAGCCCCACTCCTCCTGCGCAACCGCACTTCAGCTTGAGGCAGCCT
CACAGCCTGCCATCTGGTGCTTCCTGCCACCTGGTGCTCTCGGCTCGGTGACAGCCAACCT
GCCCTCCCCACACCAATCAGCCAGGCTGAGCCCCACCCCTGCCCCAGCTCCAGGACCTG
CCCCTGAGCCGGGCCTTCTAGTCTGAGTGCCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCA
GAGCCCCATCCCCCGCCACACCCACCGGTGGAGCTGCCTTCTCTCCCCCTCCCTCTGT
TGCCCATACTCAGCATCTCGGATGAAAGGCTCCCTTGCTCTCAGGCTCCACGGAGCGGGG
CTGCTGGAGAGAGCGGGAACTCCCAACACAGTGGGGCATCCGGCACTGAAGCCCTGGTGT
CCTGGTCAGTCCCCCAGGGGACCTGCCCCCTTCTGGACTTCGTGCCTTACTGAGTCTCT
AAGACTTTTCTAATAAACCAAGCCAGTGCCTGTAAAAAAA

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Signal sequence:

Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444

FIGURE 10

GAGCGAGGCCGGGACTGAAGGTGTGGGTGTGCGAGCCCTCTGGCAGAGGGTTAACCTGGGTC
AAATGCACGGATTCTCACCTCGTACAGTTACGCTCTCCCGCGGCACGTCCGCGAGGACTTGA
AGTCTCTGAGCGCTCAAGTTTGTCCGTAGGTGAGAGAGAAGGCCATGGAGGTGCCGCCACCGGC
ACCGCGGAGCTTTCTCTGTAGAGCATTGTGCCTATTTCCTCCGAGTCTTTGTGCGCGAAGCTG
TGACTGCCGATTCCGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCGCCAGAGCCC
TATTACCCGGAATCTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAG
AATTTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGG
TGTATGGGGGAATACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCA
GAAATTTATCATAACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTT
CATTGCTTATGGCTGGCGCTGGGGTTGGAGAACTGCAGTGTGTTGTGACTATATTCAACACAG
TGAACACTAGTCTGAATGTATACCGAAATAAAGATGCCTTAAGCCATTTTGTAAATTGCAGGA
GCTGTACACGGGAAGTCTTTTTTAGGATAAACGTAGGCCTGCGTGGCCTGGTGGCTGGTGGCAT
AATTGGAGCCTTGCTGGGCACTCCTGTAGGAGGCCTGCTGATGGCATTTCAGAAGTACGCTG
GTGAGACTGTTTCAGGAAAGAAAACAGAAGGATCGAAAGGCACTCCATGAGCTAAAACCTGGAA
GAGTGGAAAGGCAGACTACAAGTTACTGAGCACCTCCCTGAGAAAATTGAAAAGTAGTTTACG
GGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACTGCTAAACCTTCCTAGAAAAC
CTTCAGTAATAGATAAAACAAGACAAGGACTTGAAAGTGCTCTGAACTTGAAACTCACTGGAGA
GCTGAAGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCCACTCTTTGGTCAGCCTGC
TGACAAAATTTAAGTGCTGTGACCTGTGGTGGCAGTGGCTTGCTCTTGCTTTTTCTTTCTTT
TTTAACTAAGAAATGGGGCTGTGTACTCTCACTTTACTTTATCCTTAAATTTAAATACATACT
TATGTTTGTATTAACTATCAATATATGCATACATGGATATATCCACCCACCTAGATTTTAA
GCAGTAAATAAAACATTTTCGAAAAGATTAAAGTTGAATTTTACAGTTT

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FIGURE 11

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318
><subunit 1 of 1, 285 aa, 1 stop
><MW: 32190, pI: 9.03, NX(S/T): 2
MEVPPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRLRELF
GKDEQQRISKDLANICKTAATAGIIGWVYGGIPAFIHAKQQYIEQSQAIEIYHNRFDAVQSAH
RAATRGFIRYGRWGWRTAVFVTIFNTVNTSLNVYRNKDLSHFVIAGAVTGSLSLFRINVGLR
GLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDRKALHELKLEEWKGRLLQVTEHLPE
KIESSLREDEPENDAKKIEALLNLPRNPSVIDKQDKD

Important Features:

Signal Peptide:

amino acids 1-24

Transmembrane domains:

amino acids 76-96 and 171-195

N-glycosylation site:

amino acids 153-156

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FIGURE 12

CGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA
ATCTGGATGGGACCGCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGGA
CCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGAA
TACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCAT
AACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTTCGTTTCATG
GCTGGCGCCGAACC

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FIGURE 13

TCAAGTTTGTCCGTAGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGGAGCTT
TTTTCTGTAGAGCATTGTGCCTATTTCCCCGAGTTTTTGCTGCCGAAGCTGTGACTGCCGAT
TCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA
ATTTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGG
ACCTTGCTGATATNTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGA
ATACCAGCTTTTATTTCATGNTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATNA
TAACC

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FIGURE 14

GAGCCGCCGCCGCCGCCGCCGCGCACTGCAGCCCCAGGCCCGGCCCCCCACCCACGTCT
GCGTTGCTGCCCCGCTGGGCCAGGCCCAAAGGCAAGGACAAAGCAGCTGTGAGGGAACCT
CCGCCGGAGTCGAATTTACGTGCAGCTGCCGGCAACCACAGGTTCCAAGATGTTTTGCGGGG
GCTTCGCGTGTCCAAGAACATGCGCTGTGCGCCCTCAACCTGCTTTACACCTTGTTAGTCTG
CTGCTAAATTGGAATTGCTGCGTGGGGCATTGGCTTCGGGCTGATTTCCAGTCTCCGAGTGGT
CGGCGTGGTCATTGCAGTGGGCATCTTCTGTTCCTGATTGCTTTAGTGGGTCTGATTGGAG
CTGTAAAACATCATCAGGTGTTGCTATTTTTTTATATGATTATTCGTGTTACTTGTATTTATT
GTTCAGTTTTCTGTATCTTGCCTTGTTTAGCCCTGAACCAGGAGCAACAGGTCAGCTTCT
GGAGTGTGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAATCTAAACTGCT
TCGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGAGATTTGTTGG
TGGCATTGCGCTGTTCTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACCTACAGATACA
GGAACCAGAAAGACCCCCGCGCGAATCCTAGTGCAATTCCTTTGATGAGAAAAACAAGGAAT
TTCCTTTCGTATTATGATCTTGTTCACTTCTGTAATTTTCTGTTAAGCTCCATTTGCCAGT
TTAAGGAAGGAAACATATCTGGAAGTACCTTATTGATAGTGAATTATATATTTTTACT
CTATGTTTCTCTACATGTTTTTTCTTTCCGTTGCTGAAAAATATTTGAAACTGTGGTCTC
TGAAGCTCGGTGGCACCTGGAATTTACTGTATTATTGTGCGGCACCTGTCACCTGTGGCCTT
TCTTAGCATTTTTACCTGCAGAAAACTTTGTATGTTACCACTGTGTTGGTTATATGGTGAA
TCTGAACGTACATCTCACTGGTATAATTATATGTAGCACTGTGCTGTGTAGATAGTTCCTAC
TGGAAAAAGAGTGGAATTTTATTAATCAGAAAGTATGAGATCCTGTATGTTAAGGGAAA
TCCAAATTCCTAATTTTTTTTGGTCTTTTTAGGAAAGATTGTTGTTGGTAAAAAGTGTAGTA
TAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAAATAGTTAT
GTCTTAGGAAATGTGGTTTAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTGTTT
CATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCATCAGAAATGGAACGAGTTT
TGAGTAATCAGGAAGTATATCTATATGATCTTGATATTGTTTTATAATAATTTGAAGTCTAA
AAGACTGCATTTTTAAACAAGTTAGTATTAATGCGTTTGGCCCACGTAGCAAAAAGATATTTG
ATTATCTTAAAAATGTTAAATACCGTTTTTCATGAAATTTCTCAGTATTGTAAACAGCACTT
GTCAAACCTAAGCATATTTGAATATGATCTCCCATAAATTTGAAATTGAAATCGTATTGTGTG
GCTCTGTATATTCTGTTAAAAAATTAAAGGACAGAAACCTTTCTTGTGTATGCAATGTTTGA
ATTAAAGAAAGTAATGGAAG

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><subunit 1 of 1, 204 aa, 1 stop

MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFLGISSLRVVGVIAGVIGFLFLIALV
GLIGAVKHHQVLLFFYMIILLLVFIVQFSVCACLALNQEQQQGLLEVGWNNTASARNDIQR
NLNCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRFGVGGIGLFFSFTEILGVWL
TYRYRNQKDPANPSAFL

amino acids 1-34

amino acids 47-63, 72-95 and 162-182

amino acids 47-63, 72-95 and 162-182

[illegible]

TGATTTGGAGCTGTAAAAAANTCTTCAGGTTGTTGTTNATTTTTTTTATATGATTATTTCTGTAANT
 TGTATTATTGTTTCAGTTTTNTGTATCTTTCGCGCTTGTTTAGCCNTGAACCAGGAGCAACAGG
 GTCAGNTTNTGGAGGTTGGTTGGAAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAAT
 NTAAACTGCTGTGGGTTCCGAAGTGTTAAACCAAATGACACCTGTNTGGCTAGCTGTGTTAA
 AAGTGACCACTNGTCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGA
 GATTGTTTGGTGCGCATTTGGCCCTGTTNTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACC
 TACAGATACAGGAACCAG

AATCCCAAAATCCCCAATTTTTTTGGNCTTTTTAGGGAAGATGTGTTGGTAAAAAGTGT
TAGTATAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAATAG
TTATGTCCTTAGGAAATGTGGTTTAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTG
GTTTCATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCCATCAGAATGGAACG
AGTTTTGAGTAATCCAGGAAGTATATCTATATGATCTTGATATTGTTTTATATAAATTTGAAG
TCTAAAGACTGCATTTTTAAACAAGTTAGTATTAATGCGTTGGCCACGTAGCAAAAAGAT
ATTTGATTATCTTAAAAAATGTTAAATACCGTTTTTCATGAAAGTCTCAGTATTGTAAACAGC
AATCTGTCAAACCTAAGCATATTTGAATATGATCTCCATAAATTTGAAATGAAATCGTATT
GTGTGGGAAGAAATGGCAATCTTATGTGTGCTGAAGGACACAGTAAGAGCACCAAGTTGTGCC
CCACTTGC

FIGURE 18

ATGATTATTCGTACTTGTATTTATTGTTTCAGTTTTATGGTATCTTGCGCTTGTTTAGCCC
CTGAAACCAGGAGCAACAGGGNNCAGCTTCCTGGAGGTTGGTTGGCAACAATCACGGCCAAG
TGACTCCGCAAATGACATCCAGAGAAATCCTAACTGCTGTGGGTTCGGAAGTGTTAACCC
AAATGACACCTGTCTGGCTNGCTGTGTTAAAAGTGACCACTCGTGCTCGCCATGTGCTCCAA
TCATAGGAGAATATGC

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FIGURE 19

CAGTCACCATGAAGCTGGGCTGTGTCTCATGGCCTGGGCCCTCTACCTTCCCTTGGTGTG
 CTCTGGGTGGCCAGATGCTACTGGCTGCCAGTTTGTAGACGCTGCAGTGTGAGGGACCTGT
 CTGCACCTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCT
 TCCAGGTCAAGGCCCTACACTTTTCAGTGAACCCCTTCCACCTGATTGTGTCTATGACTGGCTG
 ATCTTCCAAGGTCAGCCAAGCCAGTTTTTGAAGGGGACCTGTCTGGTCTGCGCTGCCAGGC
 CTGGCAAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCC
 CCGGGCCTAACAGGGAATTCTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCACTACCAC
 TGCAGTGGCATCTTCCAGAGCCCTGGTCTGGGATCCAGAAAACAGCATCTGTTGTGGCTAT
 CACAGTCCAAGAACTGTTTCCAGCGCCAATTCTCAGAGCTGTACCCTCAGCTGAACCCCAAG
 CAGGAAGCCCCATGACCTGAGTTGTGACAGAAAGTTGCCCTGCAGAGGTGAGCTGCCCGC
 CTCTCTTCTCCTTCTACAAGGATGGAAGGATAGTGCAAGCAGGGGGCTCTCCTCAGAAAT
 CCAGATCCCCACAGCTTTCAGAAATCACTCCGGGTCTATCTGGTGTGAGGCAGCCACTGAGG
 ACAACCAAGTTTGGAACAGAGCCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCT
 GCTGCACCTCCACATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAATGCTCCTGA
 GGAGGGCCCTGGGCCTCTGCCTCCGCGCCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTT
 CTCTCTGGGGATGCCAGATCCTCATCTGTATCACCAGATGGGCTTCTTCTCAAACACATG
 CAGGATGTGAGAGTCTCTCTCGGTCACTGCTCATGGAGTTGAGGAATATCTGGCCACCA
 GAAGCCTGGGACCACAAAGGCTACTGCTGAATAGAAGTAAACAGTTTCATCCATGATCTCACT
 TAACACCCCAATAAATCTGATTTCTTTATTTTCTCTTCCTGTCTGACATATGCATAAGTA
 CTTTTACAAGTTGTGCCAGTGTTTTGTGTAAGTAATGTAGTTAGGTGAGTGTAATAAATTT
 ATATAAAGTGAGAATTAGAGTTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATTC
 TGCTGTCTAGATCAGGAATTTCTATCTGTTATATCGACCAGAATGTTGTGATTAAAGAGAA
 CTAATGGAAGTGGATTGAATACAGCAGTCTCACTGGGGGCAATTTTGCCCCCAGAGGACA
 TTGGGCAATGTTTGGAGACATTTTGGTCATTATACCTGGGGGGTGGGGGATGGTGGGATGT
 GTGTCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCGGCTAAACATCCTATAATGCACAG
 GGCAGTACCCACAACGAAAAATAATCTGGCCCAAAATGTCAGTTGTACTGAGTTTGAGAAA
 CCCCAGCCTAATGAAACCCCTAGGTGTTGGGCTCTGGAATGGGACTTTGTCCTTCTAATTAT
 TATCTCTTTCCAGCCTCATTCAGCTATTCTTACTGACATACCAGTCTTTAGCTGGTGTATG
 GTCTGTTCTTTAGTTCTAGTTTGTATCCCTCAAAGCCATTATGTTGAAATCCTAATCCCC
 AAGGTGATGGCATTAAAGAGTGGGCCTTTGGGAAGTGATTAGATCAGGAGTGCAGAGCCCTC
 ATGATTAGATTAGTGCCCTTATTTAAAAAGGCCCAGAGAGCTAACTCACCTTCCACCAT
 ATGAGGACGTGGCAAGAAGATGACATGTATGAGAACCAAAAAACAGCTGTGCGCAACACCG
 ACTCTGTCTGTGCTTGTATCTTGAACCTCCAGCCTCCAGAACTATGAGAAATAAAATCTGG
 TTGTTGTAGCCTAA

09978564-301609

FIGURE 20

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594
><subunit 1 of 1, 359 aa, 1 stop
><MW: 38899, pI: 5.21, NX(S/T): 0
MKLGCVLMAWALVLSLGVLWVAQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQV
KAYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRQAWQDWPLTQVTIFYRDGSALGPPGP
NREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGS
PMTLSCQTKLPLQRSAAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQ
VWQSPQLEIRVQGAASSAAPPTLNPAPOKSAAPGTAPEEAPGPLPPPPPTPSSSEDPGFSSPL
GMPDPHLYHQMGLLLKHMVDVRVLLGHLLMELRELSGHQKPGTTKATAE

Signal sequence:

amino acids 1-17

Leucine zipper pattern sequence:

amino acids 12-33

Protein kinase C phosphorylation site:

amino acids 353-355

09978564-11601
TOTTI-498/660

FIGURE 21

CCCACGCGTCCGCCACGCGTCCGCCACGGGTCCGCCACGCGTCCGGGCCACCAGAAGTT
 TGAGCCTCTTTGGTAGCAGGAGGCTGGAAGAAAGGACAGAAGTAGCTCTGGCTGTGATGGGG
 ATCTTACTGGGCCTGTACTCTTGGGGCACCTAACAGTGGACACTTATGGCCGTCCCATCCT
 GGAAGTGCCAGAGAGTGTAAACAGGACCTTGGAAAGGGGATGTGAATCTTCCCTGACACCTATG
 ACCCCCTGCAAGGCTACACCCAAGTCTTGGTGAAGTGGCTGGTACAACGTGGCTCAGACCCCT
 GTCACCATCTTTCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCAAAGTACCAGGGCCG
 CCTGCATGTGAGCCACAAGGTTCCAGGAGATGTATCCCTCCAATTGAGCACCCCTGGAGATGG
 ATGACCGGAGCCACTACAGTGTGAAGTCACTGGCAGACTCCGTGATGGCAACCAAGTCTGTG
 AGAGATAAGATTACTGAGCTCCGTGTCCAGAACTCTCTGTCTCCAAGCCCACAGTGACAAC
 TGGCAGCGGTTATGGCTTCACGGTGGCCAGGGGAATGAGGATTAGCCTTCAATGCCAGGCTC
 GGGGTTCTCCTCCATCAGTTATATTTGGTATAAGCAACAGACTAATAACAGGAACCCATC
 AAAGTAGCAACCCTAAGTACCTTACTCTTCAAGCCTGCGGTGATAGCCGACTCAGGCTCCTA
 TTTCTGCACTGCCAAGGGCCAGGTTGGCTCTGAGCAGCACAGCGACATTGTGAAGTTTGTGG
 TCAAAGACTCCTCAAAGCTACTCAAGACCAAGACTGAGGCACCTACAACCATGACATACCCC
 TTGAAAGCAACATCTACAGTGAAGCAGTCTCTGGGACTGGACCACTGACATGGATGGTACCT
 TGGAGAGACCAGTGCTGGGCCAGGAAAGAGCCTGCTGTCTTTGGCCATCATCTCATCATCT
 CCTTGTGCTGTATGGTGGTTTTTACCATGGCCTATATCATGCTCTGTGCGAAGACATCCCAA
 CAAGAGCATGTCTACGAAGCAGCCAGGTAAAGAAAGTCTCTCCTCTTCCATTTTTGACCCCGT
 CCCTGCCCTCAATTTTGATTACTGGCAGGAAATGTGGAGGAAGGGGGGTGTGGCCACAGACCC
 AATCTTAAGGCCGGAGGCCCTTCAAGGTCAGGACATAGCTGCCTTCCCTCTCTCAGGCACCTT
 CTGAGGTTGTTTTGGCCCTCTGAACAACAAGGATAATTTAGATCCATCTGCCTTCTGCTTCC
 AGAATCCCCTGGGTGGTAGGATCCTGATAATTAATTGGCAAGAATTGAGGCAGAAGGGTGGGA
 AACCAGGACCAAGCCCCAAGTCCCTTCTTATGGGTGGTGGGCTCTTGGGCCATAGGGCACA
 TGCCAGAGAGGCCAACGACTCTGGAGAAACCATGAGGGTGGCCATCTTCGCAAGTGGCTGCT
 CCAGTGATGAGCCAACTTCCAGAATCTGGGCAACAACCTACTCTGATGAGCCCTGCATAGGA
 CAGGAGTACCAGATCATCGCCAGATCAATGGCAACTACGCCCCGCTGCTGGACACAGTTCC
 TCTGGATTATGAGTTTCTGGCCACTGAGGGCAAAAGTGCTGTGTTAAAAATGCCCATTAGGC
 CAGGATCTGCTGACATAATTGCCCTAGTCAGTCTTGCCTTCTGATGGCCTTCTTCCCTGCT
 ACCTCTCTTCTGGATAGCCCAAAGTGTCGCTTACCAACACTGGAGCCGCTGGGAGTCACT
 GGCTTTCCTTGGAAATTTGCCAGATGCATCTCAGTAAGCCAGCTGCTGGATTTGGCTCTGG
 GCCCTTCTAGTATCTCTGCCGGGGGCTTCTGGTACTCCTCTCTAAATACCAGAGGGAAGATG
 CCCATAGCACTAGGACTTGGTCATCATGCCTACAGACACTATTCAACTTTGGCATCTTGCCA
 CCAGAAGACCCGAGGGAGGCTCAGCTCTGCCAGCTCAGAGGACCAGCTATATCCAGGATCAT
 TTTCTTTTCTTCAGGGCCAGACAGCTTTAATTGAAATTTGTTATTTTACAGGCCAGGGTTCA
 GTTCTGCTCCTCCACTATAAGTCTAATGTTCTGACTCTCTCCTGGTGTCTCAATAAATATCTA
 ATCATAACAGC

09978564-101601

FIGURE 22

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45416

><subunit 1 of 1, 321 aa, 1 stop

><MW: 35544, pI: 8.51, NX(S/T): 0

MGILLGLLLGLHLLTVDTYGRPILEVPESVTGPWKGDVNLPCITYDPLQGYTQVLVKWLVQRGS
DPVTIFLRDSSGDHIQQAKYQGRLEVSHKVPDVSLLQLSTLEMDDRSHYTCEVTWQTPDGNQ
VVRDKITELRVQKLSVSKPTVTGSGYGFTVPQGMRLSLQCQARGSPPISYIWKQQTNNQE
PIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKTEAPTTMT
YPLKATSTVKQSWDWTDDMDGYLGETSAGPGKSLPVFAILLIISLCCMVVFTMAYIMLCRKT
SQQEHVYEAAR

Signal Sequence:

amino acids 1-19

Glycosaminoglycan attachment site:

amino acids 149-152

Transmembrane domain:

amino acids 282-300

007551-1058260

FIGURE 23

GCGCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGCGGGGCCGGCTCCCGCCCGGCACAT
 GGCTGCAAGCCACCTCGCGCGCACCCGAGGCGCGCGCCAGCTCGCCCGAGGTCCGTGCGA
 GCGCCCGCGCGCCCGGAGCCAGCAGCAACTGAGCGGGGAAGCGCCGCGCTCCGGGGATC
 GGGATGTCCTCCTCCTTCTCCTCTTGCTAGTTTCCTACTATGTTGGAACTTTGGGGACTCA
 CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCCTGCCACCATCAACTGGGGC
 TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGAAACCAAAAA
 GTGGTGATCACTTACTCCAGTCGTCTATGTCTACAATAACTTGACTGAGGAACAGAAAGGCCG
 AGTGGCCTTTGGCTTCCAATTTCTGGCAGGAGATGCCTCCTTGAGATTGAACCTCTGAAGC
 CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTACAGGGCGCTACGCTGTGGAGCCAT
 GTCATCTTAAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC
 AGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTTGTGTATT
 ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCTCCCAAATCTAGGATT
 GACTACAACCACCTTGGACGAGTTCTGCTGCAGAATCTTACCATGTCTTACTCTGGACTGTA
 CCAGTGCAAGCAGGCAACGAAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAACTGTACAGT
 ATGTACAAGCATCGGCATGGTTGCAAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG
 ATTTTCTCTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA
 GAGACCTAATGAAATTGAGAAGATGCTGAAGCTCCAAAGCCGCTCTTGTGAAACCCAGCT
 CCTCTCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCTCCACTCGCTCCACAGCAAAAT
 AGTGCCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCAC
 CCAGGCTACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAAACCAAGAAAGTCCACCATG
 CTAATCTGACCAAAGCAGAAACCAACACCCAGCATGATCCCGCAGCAGAGCAGCTTCCAA
 ACGGTCGTAATTACAATGGACTTGACTCCCACGCTTTCTAGGAGTCAGGGTCTTTGGACTC
 TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCCAGATGAGAGGTCACTTAAGTAGCA
 GTGAGCATTGACGGAACAGATTGAGATGAGCATTTTCTTATACAATCCAAACCAAGCAAA
 AGGATGTAAGCTGATTTCATCTGTAAAGGAGCATCTTATTGTGCTTTAGACCAAGAGTAAGGG
 AAAGCAGGAGTCCAATCTATTTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG
 AGGTGAATATACCTAAAACTTTTAAATGTGGGATATTTGTATCAGTGCTTTGATTACAATT
 TTCAAGAGGAAATGGGATGCTGTTGTAAATTTTCTATGCACTTTGCAAACTTATTGGATT
 ATTAGTTATTGACAGACTCAAGCAGAACCCACAGCCTTATTACCTGTCTACACCATGTAC
 TGAGCTAACCACTTCTAAGAACTCCAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC
 TTCATTTGTCTAAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA
 AGAGTGAATGAGTTTCTCCACTCTATACTAATCTCACTATTGTATTGAGCCCAAAATTAAC
 TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCCATCTCTCATGATGT
 ATGAGGATTGTTGACAAACATTAGAATATATATAATGGAGCAATTGTGGATTTCCTCAAT
 CAGATGCTCTAAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAAAATACAACATGTCAAT
 TATCAACGTCTTTAGAAAGAACTCTTAGAGAAAAAGGGATCTAGGAATGCTGAAAGATTGA
 CCCAATCCTTATAGCTCTCTTCTTTCTGAGAAATGTGAAACCAAGAAATTGCAAGACTTG
 GTGGACTAGAAGGGAGATTGATCAGTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA
 TGGTGCCAGGACCTGTAGGAAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC
 ATTGCACTCCAGCTGGGTGACAGAGCGGACTCCGCTC

09978564-101501

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYVGTLGTHTEIKRVAAEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVNSHV
ILKVLVRPSKPKCELEGELTEGSDLTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVRVTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPPSSSSSGSRSSRSGSSSTRSTANS
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

0007554.10360
109701.495260

FIGURE 25

GTCGTTCCTTGTCTCTCGCGCCAGTCTCTCTCCCTGGTTCTCTCTCAGCCGTGTGCGAGGAGAGACCCCGGA
 GACGCGGGCTGAGTGTGCGCGGCTTCTCCCGCCTGGGGCGGCTCGCGCTGGGCGAGTGTCTGAGCGCCCTAG
 AGCCTTCCTTGGCGGCTCTCTCTCTGCGCGCGCGCAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCG
 GCCCGGGAGGCGGGGTGGATGCGGCGCTGGGCGAGAGCAGCGCGGATTCCAGCTGCCCGCGCGCGCGCGGGG
 CCCCCTGCGAGTCCCCGGTTACGCCATGGGGACCTCTCCGAGCAGCAGCAGCGCCCTCGCCTCTCTGAGCGGCATC
 GCGCGCTGAGCCACAGCCACGATGATCGCGGGCTCCCTTCTCTGCTTGGATTCTTAGCACCACACAGCTCAG
 CCAGAACAGAAAGGCTCGAATCTCATTTGSCACATACCCCGATGTGACCGTGTGACCGTGGCAGGTGCTAACCTGT
 GACAAAGTGTCCAGCAGAACCTTATGTCTCTGAGCACTGTACCAACACAAGCCTGCGCGCTCTGAGCAGATTGCGCT
 GTGGGGACCTTTACCAGGCATAGAAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGTGCCATGGCCAAATG
 ATTGAGAAATTAATCTGTGCTGCTGACTGACCCAGAAATGCACTTGGCCACCTGGCATGTTCAGTCTTCAACGCT
 ACTGTGCGCCCCCATACCGTGTGCTGTGCTGTGGGTGTGCGGAAGAAAGGAGACAGAGACTGAGGATGTGCGG
 TGTAAGCATGTGCTCGGGGTACTTCTCAGATGTGCTTCTAGTGTGATGAAATGCAAGCATACACAGACTGT
 CTGAGTCAGAACTTGGTGTGATCAAGCGCGGGACCAAGGAGACAGACACGCTCTGTGGCACCTCCCGTCTCTT
 TCCAGCTCCACCTCACCTTCCCTGGCAGAGCCATCTTTCCAGCGCCTGAGCACATGGAAACCCATGAAGTCCCT
 TCTCCACTTATGTGTCCAAAGGCATGAATCAACAGAAATCCAATCTTCTGCTCTGTGTAGACAAAGGTAATG
 AGTAGCATCCAGGAAGGACAGTCCCTGACACACAAGCTCAGCAGGGGGAGGAAGACGTAAGAACAGACCCCTC
 CCAACCTTCAGGTAGTCAACCAACAGCAAGGCCCCACACAGACATCTGAGGAGCTGCTGCGCTCCATGGAG
 GGCATGGGGCGGAGAGTCCAGCAGCGCCCATCAAGGGCCCCAAGAGGGGACATCTAGACAGAACTTACACAG
 CATTTTGAATCAATGAGCATTTGCCCTGGATGATTGTGCTTTTCTGCTGTGGTGTGTGGTGTGATTGTGGTG
 TGCAGTATCCGGAAGAGCTCGAGGACTGTGAAAAAGGGGCCCCCGCAGGATCCAGTGGCATTTGTGGAAAGGCA
 GGGCTGAAGAAATCCATGACTCAACCCAGAACCGGGAGAAATGGATCTACTACTGCAATGGCCATGGTATCGAT
 ATCCTGAAGCTTTAGCAGCCCAAGTGGGAAGCCAGTGGAAAGATATCTATCAGTTCTTTGCAATGCCAGTGGAG
 AGGGAGGTTGCTGCTTTCTCAATGGGTACACAGCGGACACAGGCGGGCTACGAGCTCTGCAGCATGTGAGC
 ATCCGGGGCCCCGAGGCGAGCTCGCCAGCTAATTAGCGCCCTGCGCGACACCGGAGAACGATGTTGTGGAG
 AAGATTCTGGGTGTGAGGAAGACACACCCAGCTGGAAACTGACAACTAGCTCTCCCGATGAGCTCCAGCCCG
 CTTAGCCGAGCCCATCCCGAGCCCAACGCGAAACTTGAGAAATCCGCTCTCTGACGCTGGAGCTTCCCCA
 CAGGACAAGAACAGGGCTTCTGTGGATGAGTCGGAGCCCTTCTCCGCTGAGCTCTCATATCCAGCGCTCC
 TCCGCGCTGAGCAGGAACGGTTCCTTTATTAACAAAGAAAGAGGACACAGTGTGCGCAGGTACGCTGGAC
 CCGTGTGACTTGCAGCTATCTTTGATGACATGCTTCACTTCTTAATCTGAGGAGCTGCGGGTGTATTAAGAG
 ATTCCCCAGGCTGAGGACAACTAGACCGGCTATTGGAATTAATTGAGTCAAGAGCCAGGAAGCCAGCAGCC
 CTCTGGACTCTGTTTATAGCCATCTTCTGACCTGCTGTGAGAACATAGGATATGCTATTCTGAAATTAATCA
 ATTTAGTGGCAGGGTGGTTTTTAATTTCTCTGTCTTCTGATTTTGTGTGTGGGGTGTGTGTGTGTGTGT
 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTAACAGAAATATGGCAGTGTCTTGAGTTCTTTCTCTCTCTC
 TCTCTCTCTTTTTTTAAATAACTCTTCTGGAGTGTGGTTTATAGAGCTTTTCCATCTTTATGATTTTCAAGATTATCTG
 ATACCCACCATTAAGGTTTCTTTAAGTTCATATTTCTCCATTTTGTCTTTTATGATTTTCAAGATTATCTG
 TGCATCTTAAATTTACTTAACCTTACATAAATGCAAGTGTGACTTTTCCACACACTGGATGTGAGGCTCTTAA
 TCTCTTAAAGATTAATGGCCTCTTGTGAATCTTATAGCAGTCTTTATGTCTCTTAACATTCAACCTACTTTTT
 AAAAAACAAATTAATTAATTTTATTTATTTGTTGTCTTTTATAAATTTCTTAAAGATTAAGAAAAATTTAAGA
 CCCCATTGAGTACTGATTAATGCAATCACTTTGAGTTATCTTTTAAATATGTCTTGTATAGTTTCAATATCATGG
 CTGAAACTTGACACATCTCTGCTGAGTGTGAGAAATGCTCAAGCCATCAGGATTTGCTATTTAAGTGGCTT
 TCTTCTTATGCTAATATGCTGCGCTGGAGAAATGAAATCTCAAGCCATCAGGATTTGCTATTTAAGTGGCTT
 GAAAGTCAACCAATCAAGTGGCAGTGGCGCCCTTCCATAGAGAAATTTGCCAGCTTTGCTTTGGAACACATTTGCTGCACTT
 TTTTTATATACACATTAATCAATAGGTCCAATCTGCTCTCAAGGCTTGGTCTGGTGGGATCTCTTCAACAAAT
 TACTTTAATTAAGAGTGGCTGCACTGTGAAGAACCTTTGCTGATATATTGCAACATATGCTCCCATTTACAAATG
 TACCTTCTAATGCTGAGTGGCGGTTTCAATGCAAGGTGGCGTGGACTCCCTTTGTGTGGTGGGGTGTGTGG
 GTAGTGTGAGGACCGATATCAGAAAAATGCTTCAAGTGTACTAATTTATTAATAAACATTAGGTGTGTGTA
 AAAAAAAA

097854.10160

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><subunit 1 of 1, 655 aa, 1 stop
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[illegible]

amino acids 1-41

amino acids 350-370

FIGURE 27

ATGGGAAGCCAGTAACACTGTGGCCCTACTATCTCTTCCGTGGTGCCATCTACATTTTTTGGGA
 CTCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTCAGAGGTCCTGAAATAGTCAC
 CATGGGGGAAAAATGATCCGCTGCTGTTGAAGCCCCCTTCTCATTTCCGATCGCTTTTTGGCC
 TTGATGATTTGAAAAATAGTCCTGTGTGCACCAGATGCAGATGCTGTTGCTGCACAGATCCTG
 TCACCTGCTGCCATTGAAGTTTTTTTCCAATCATCGTCATTGGGATCATTGCATTGATATTAGC
 ACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTACAGATGTGCTCATCCT
 TTAAGTGTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAGAGCGGGAGGAC
 GAGTACCGCTGTGCTCCGGGTGGTGGTCAAGTGCCGTCTCAGGTGTTTCAAGGTGCTTC
 GTGGAAGACCATGTGCTCCGATGACTGGAAGGGTCACTACGCAATGTTGCTGTGCCAAC
 TGGGTTTCCCAAGCTATGTGAGTTAGATAACCTCAGAGTGAGCTCGCTGGAGGGGAGTTT
 CGGGAGGAGTTTGTGTCCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCA
 CTCAGTATATGTGAGGGAGGGATGTGCCCTGTGCCACGTTGGTTACCTTGCAGTGACACGCC
 GTGGTCATAGAAAGGGCTACAGCTCACGCATCGTGGGTGGAACATGTCCTTGCTCTCGAG
 TGGCCCTGGCAGGCCAGCCTTCAGTTCCAGGGTACCCTGTGCGGGGCTCTGTGCATCAC
 GCCCTGTGGATCATCACTGCTGCACACTGTGTTTATGACTTGTACCTCCCAAGTCATGGA
 CCATCCAGGTGGGTCTAGTTTCCCTGTTGGACAATCCAGCCCCATCCCACTTGGTGGAGAAG
 ATTGTCTACCACAGCAAGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCT
 GGC CGGGCCACTCAGCTTCAATGAAATGATCCAGCCTGTGTGCTGCCAAGCTCTGAAGAGA
 ACTTCCCGATGGAAAAGTGTGCTGGACGTCAAGATGGGGGGCCACAGAGGATGGAGGTGAC
 GCCTCCCTGTCTGTAACCAACGCGGCGCTCCCTTGTATTTCCAACAAGATCTGCAACCCACAG
 GGACGTGTACGGTGGCATCATCTCCCTCCCTCAATGCTCTGCGCGGGCTACCTGACGGGTGGCG
 TGGACAGCTGCCAGGGGGACAGCGGGGGCCCTGTGTGTCAAGAGAGGAGGCTGTGGAAG
 TTAGTGGGAGCGACCAAGCTTTGGCATCGGCTCGCCAGAGGTGAACAAGCCTGGGGTGTACAC
 CCCTGTCACTCCTTCTCTGGACTGGATCCACGAGCAGATGGAGAGAGACCTAAAAACCTGAA
 GAGGAAGGGGACAAGTAGCCACCTGAGTTCTGAGGTGATGAAGACAGCCCGATCCTCCCT
 GGACTCCCGTGTAGGAACCTGCACACGAGCAGACACCTTGGAGCTCTGAGTTCCGGCACCA
 GTAGCAGGCCCGAAAGAGGCCACCTTCCATCTGATTCAGCACAACTTCAAGCTGCTTTTT
 GTTTTTTTGTTTTTTTGGAGTGGAGTCTCGCTCTGTTGCCCAGGCTGGAGTGCAAGTGGCGAAA
 TCCCTGCTCACTGCAGCCTCCGCTTCCCTGGTTCAAGCGATTCTCTGCTCAGCTTCCCCA
 GTAGCTGGGACCACAGGTGCCCGCCACCACACCCAACTAATTTTTTGATTTTTTAGTAGAGAC
 AGGTTTTACCATGTTGGCCAGGCTGCTCTCAAACCCCTGACCTCAAATGATGTGCTGCTGCT
 CAGCCTCCCACAGTGTCTGGGATTACAGGCATGGGCCACACGCCCTAGCTCACGCTCCTTTC
 TGATCTTCACTAAGAACAAAGAAAGCAGCAACTTGCAGGGCGGCCCTTCCCACTGGTCCAT
 CTGTTTTCTCTCCAGGCTCTGCAAAATTCCTGACGAGATAAGCAGTTATGTGACCTCAG
 TGCAAGCCACCAAGCCACTCAGAAAAGACGACCCAGCCAGAAAGTGACAGAACTGCAGT
 ACTGCACGTTTTTATCTCTAGGGACCAGAACCAACCCACCTTCTACTTCCAAGACTTAT
 TTTTCAATGTGGGGAGGTTAATCTAGGAATGACTCGTTTAAAGCCCTATTTTCATGATTTCTT
 TGTAGCATTTGGTGTCTGACGTATTATTGTCTTTGATTCCAAATAATATGTTTCTTCCCT
 CATGTCTGGCGTGTCTGCGTGGACTGGTGACGTGAATCAAATCATCCACTGAAA

0978564.101601

FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234

><subunit 1 of 1, 453 aa, 1 stop

><MW: 49334, pI: 6.32, NX(S/T): 1

MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLPLKFFPIIVIGIILILA
LAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVFTAAS
WKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIHLLPDDKVLTALHH
SVYVREGCASGHVVTLOCTACGHRRGYSSRIVGGNMSLLSQNPWQASLQFQGYHLCGGSVIT
PLWIITAACHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKL
AGPLTFNEMIQPVCLPENSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAVPLISNKICNHR
DVYGGIISPSMLCAGYLTGGVDSQCQDGGGLVCQERRLWKLVGATSPFGIGCAEVNKPQVYT
RVTSFLDWIHEQMERDLKT

Signal Peptide:

amino acids 1-20

Transmembrane domain:

amino acids 240-284

0970591-101601

FIGURE 29

CCCACGCGTCCGTCTAGTCCCCGGGCCAACTCGGACAGTTTGTCTCATTATTATGCAACGGTCAAGGCTGGCTTGT
 GCCAAGACGCGCGCGCGCGCGGCGCACGACGACACACACGCGGGGGAACTTTTTTAAAAATGAAGGCTAGAGAGA
 GCTCAGCGCGCGCGCGCGCGCGCTCGCGGAGGCTCCGGAGCTGACTCCCGAGGCGAGGAATCCCTCGGTTCGCGA
 CGCCCGCGCCCGCTCGCGCGCGCGCTGGGATGGTGACGCGCTCGCCGCGGGCCGAGAGCTGCTGCATCGGAAG
 GCCGCGGACATGCGAGCGCGCGCGCTGCCGTGTCCCCGCCCGCGCCCTCTGTCTCCGCTGGCGCGGTGCTCT
 GCTCGCGCTCGCGAGGCGCGAGGGGTGAGCTTATGGAACCAAGGAAGAGCTGATGAAGTTGTCAAGTGCCTCTGT
 TCGGATGGGAGCCTCTGGATCCCACTGAAGAGCTTCGACTCCAAGATCATCCAGAAGTGTCTGAATATTTCGACT
 ACAACGCGGAAGCAAGAGACTGATCATAAATCTGGAAGAAAGTAAGGTTCTCATTGCCAGCAGTTTCAAGCAAC
 CCACCTATCTGCAAGACGGTACTGATGTCTCCCTCGCTCGAAATTACAAGGTCACGTGTTACTACCAATGGACATGT
 ACAGGCAATCTGATTCAGCAGTCACTGACACGTTCTGTCTCGAGGACTTTATGTGTTTGAAGATGA
 AAGCTATGTCTTAGAACCAATGAARAAGTGCAACCAACAGATACAAACTCTCCAGCGAAGAAAGCTGAAAGCGT
 CCGGGGATCATGTGGATCATACACACACCAAACTCGCTGCAAGAAATGTGTTCCACCAACCTCTCAGAC
 ATGGGCAAGAGGCATAAAAGAGAGACCTCAAGGCAACTAAGTATGTGGAGCTGGTGTCTGGGCGAGCAACCG
 AGAGTTTCAGAGGCAAGGAAAAGATCTGGAAGAAAGTTAAGCAGCGATTAAAGAGATTTGCTAATCACGTGACAA
 GTTTTACAGACCATCTGAACATTTCGGATCGTGTGGTAGGCGTGGAGTGTGAATGACATGGACAAATGCTCTGT
 AAGTCAGGACCCATTACAGCCTCCATGAATTTCTGGACTGGAGGAAGATGAAGCTTCTACCTCGCAATCCCA
 TGACAATGCGCAGCTTGTCACTGGGGTTTATTCCAAAGGACCAACCATCGGCGATGGCCCCAATCATGAGCATGTG
 CACGCGACACCACTCTGGGGGAATTTCTCATGGACCATCAGACAAATCCCTTGGTGACGCGTGAACCTGGCA
 TGAGCTGGGCGCAAAATTTCCGGGATGAATCATGACACACTGGACAGGGGCTGTAGCTGTCAATGGCGGTTGAGAA
 AGGAGGCTGCATCATGAACCTTCCACCGGTACCCATTTCCATGGTGTTCAGCAGTTGTCAGCAGGAAGACTT
 GGAGACCACTCGGAGAAAGGAATGGGGGTGTGCTGTTTAACTCGCGGAAGTCAGGGAGTCTTTCGGGGCCCA
 GAAGTGTGGGAACAGATTTGTGGAAGAAGGAGAGGAGTGTGACTGTGGGGAGCGAGGAAGTATGAATCGCTGT
 CTGCAATGCCACCACTGTACCTGAAGCGGACGCTGTGTGCGCACATGGGCTGTGCTGTGAAGACTGACCGCT
 GAAGCCTGCGAGGAACAGCGTGCAGGACTCCAGCAACTCTGTGACCTCCAGAGTCTGTCAGAGGGGCGAGCCCT
 TCACTGCCAGCGCAATGTGTACTGACGATGGGCACTCATGTCAGGATGTGGAAGCTCTGCTACTGCTCAATGGCAT
 CTGCGAGACTCAGAGCAGCAGTGTGTCACTGTGGGACCAAGTGTCAAACTCCCTCGGATGCTCTGTTGA
 GAGAGTCAATTTCTGAGGTGATCTTATGGCACTGTGGCAAACTCTCGAAGAGTCTGCTTGTCAAAATGCGAGAT
 GAGAGATGCTAAATGTGGAAGAAATCCAGTGTCAAGGAGTGCAGCCCGGCGAGTCAATGGTACCAATGCGGTTTC
 CATAGAAACAAACTCCCTCTGCGCAAGGAGGCGGATTTCTGTCCGGGGGCCACCGTGTACTTGGGCGATGA
 CATCGCGGACCCAGGGCTGTGCTGTGACGCAAAAGTGTGCAATGGAATGGAAGTGTGCAACCAACAGGAGAA
 CTGCCACTGCGAGGCCACTGGGCACTCCCTCTGTGCAAAAGTTGGCTTGGAGGAAGCAAGACAGCAGCGGCC
 CATCGGCAAGCGAGCAAGCAAGGCAAGCTGCAAGTGTCAACAGGAGGCGCGGCCAGGGCCAGAGAGCCCGTGG
 ATCGCAGGAGACTGCTCTACTGCTCTCACTGACACTCATCTGAGGCCCTCCCATGACATGGAGACCGTGAACAGT
 CTGCTCAGAGGAGTGTCACTGCTGCGCTCCCGAGGCTCTGCTGACTGGCAGCATGACTCTGTGGCTTTGCCATCGT
 TCCATGACACAGACCAACACAGTTCTCGGGCTCAGGAGGGGAGTCCAGCTTACCAAGGCGCTCTGCGAGAA
 CAGTGCAGGAGGAGGCGACCATCTCTGTGTGAGCTTCTGCTAAAACATGGACATGCTTCAAGTGTCTGCTGAG
 AGAGTGCAGTGTACCACTCTGGGAGCCCGAGCCCTGCGACAGGAGGAAGAGACTCAAAAGTCTGGGCTTTC
 ACTGAGCTCCACAGCAGTGGGGGAGAGCAAGGGTTGGGCCAGTGTCCCTTTCCCACTGACACCTCAGCCT
 TGGCAGCCTCTGATGACTGCTCTCTGGCTGCACTTAATGCTCTGATATGCTTTAGCATTTATTTATGAAAT
 AGCAGGTTTATGTTTATTTATTCAGAGACCTTGCCACCAATTCATCTCCATCCAAGCAAAGTGAATGGCA
 TGAACAACTGTGAGAAAGAGTGAAGAAAGGGCGGTGAATCTTGTCTGTGACATGCTGTGACATGCTGTGAC
 AGTACTCAGGTTTGAAGGGTTTGCAGAAAGCCAGGGAACCCACAGAGTCAACCACTCTCATTTAAACAGATGAAGA
 TTGTAAAAGTGAACAACTGTGAAGGCTTAATCTCAATCCCGTGGCCATTACTGATATAAATAGAGTGCATTT
 GAAT

09978564.101601

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624

><subunit 1 of 1, 735 aa, 1 stop

><MW: 80177, pI: 7.08, NX(S/T): 5

MAARPLFPVSPARALLLAGALLAPCEARGVSLWNQGRADEVVSASVRSGLWIPVKSFDSK
NHPEVLNIRLQRESKELIINLERNEGLIASSFTETHYLQDGTDVSLARNYTGHCYYHGHVRG
YSDSAVSLSTCSGLRGLIVFENESYVLEPMKSATNRYKLFPAKKLKSVRGSCGSHHNTPNLA
AKNVFPFPPSQTWARRHKRETLKATKYVELVIVADNREFQRQGDLEKVKQRLIEIANHVDKF
YRPLNIRIVLVGVEVWMDMKCSVSQDPFTSLHEFLDWRKMKLLPRKSHDNAQLVSGVYFQG
TTIGMAPIMSMCTADQSGGIVMDHSDNPLGAAVTLAHELGHNFGMNHDTLDRGCSCQMAVEK
GGCIMNASTGYPPFMVFSSCSRKDLETSLEKGMGVCLFNLPEVRESFGGQKCGNRPFVEEGEE
CDCGEPEECMNRCNATTCITLKPDVCAHGLCCEDQLKPAGTACRDSSNSCDLPEFCTGAS
PHCPANVYLHDGHSCQDVGDCYNGICQTHEQQCVTLWGPAGKAPAGICFERVNSAGDPYGN
CGKVSKSSFAKCEMRDAKCGKIQCGGASRPVIGTNAVSIETNIPLOQGGRI LCRGTHVYLG
DDMPDPGLVLAGTKCADGKICLNRCQNISVFGVHECAMQCHGRGVCNNRNKNCHCEAHWAPP
FCDKFGFGGSTDSGPIRQAEARQEAESNRERGGQGEFVGSQEHASTASLTILI

Signal peptide:

amino acids 1-28

FIGURE 31

TCCCAAGGCTTCTTGGATGGCAGATGATTTNTGGGGTTTTGCATTGTTTTCCCTGACAACGAAA
ACAAAAACAGTTTTTGGGGGTTT CAGGAGGGGAANTCCAGCCTACCCAGGAAGTTTGCAGAAACA
GTGCAAGGAAGGGCAGGANNTTCTGGTTGAGNTTTTTGNTAAAAACATGGACATGNTTCAGTG
CTGCTCNTGAGAGAGTAGCAGGTTACCACTTTTGGCAGGCCCCAGCCCTGCAGCAAGGAGGA
AGAGGACTCAAAAGTTTGGCCTTTCACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTT
GGGCCCAGTGTCCTCTTCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATAACTGGTNTNT
GGCTGCAANTTAATGCTNTGATATGGCTTTTAGCATTTATTATATGAAAAATAGCAGGGTTTT
AGTTTTTAATTTATCAGAGACCCCTGCCACCCATTCCATNTCCATCCAAG

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[illegible]

FIGURE 33

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48309

><subunit 1 of 1, 67 aa, 1 stop

><MW: 6981, pI: 7.47, NX(S/T): 0

MGKGMVAMLILGLLLLALLLPVQVSSFVPLTSMPEATAAETTKPSNSALQPTAGLLVLLAL
LHLYH

Signal peptide:

amino acids 15-27

097864.10401

ENTER THE 1950s

[illegible]

FIGURE 35

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47629, pI: 5.90, NX(S/T): 0
MPARPGRLLPLLARPAALTALLLLLGHGGGGRWGARAQEAAAAAADGPPAADGEDGQDPHS
KHLYTADMFTHGIQSAAHFVMFFAPWCGHCQRLQPTWNDLGDKYNSMEDAKVYVAKVDCCTAH
SDVCSAQGVRGYPTLLKLFKPGQEAVKYQGPRDFQTLLENWMLQTLNEEPVTPEPEVEPPSAFE
LKQGLYELASNFELHVAQGDHFIFKFFAPWCGCHKALAPTWEQLALGLEHSETVKIGKVDCT
QHYELCSGNQVRGYPTLLWFRDGKKVDQYKGRDLESLEYVESQLQRTETGATETVTPSEA
PVLAAEPEADKGTVLALTENNFDITIAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLA
GVKIAEVDCTAERNICSKYSVRGYPTLLLFRRGGKKVSEHSGGRDLDSLHRFVLSQAKDEL

Signal sequence:

amino acids 1-32

0978554-101601

FIGURE 36

CTTTTCTGAGGAACACAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTAT
CCTCCTGGTACTATTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCCTA
CCGCTGAAGTCTGTGCCACACACAATTTACCAGGACCCAAAGGAGATGATGGTGAAAAA
GGAGATCCAGGAGAAGAGGGAAAGCATGGCAAAGTGGGACGCATGGGGCCGAAAGGAATTAA
AGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGA
AGGGTGACAAAGGGGAAAAAGGTTTGCTTGGAATACCTGGAGAAAAAGGCAAAGCAGGTACT
GTCTGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACCTGGATATTAGTATTGCTCGGCT
CAAGACATCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAAACTGAAGAGAAAT
TCTACTACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGG
GGTGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGC
CAAGAGTGGCTTCTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAAGGGAGGGACAGTACA
TGTCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCGAC
CCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG
CCATCTTACCATGTACTTTGTCTGTGAGTTCATCAAGAAGAAAAAGTAACTTCCCTCATCCT
ACGTATTTGCTATTTTCTGTGACCGTCATTACAGTTATTGTTATCCATCCTTTTTTTCCTG
ATTGTACTACATTGTGATCTGAGTCAACATAGCTAGAAAATGCTAAACTGAGGTATGGAGCCT
CCATCATCAAAAAAAAAAAAAAA

09978554.101601

FIGURE 37

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980

><subunit 1 of 1, 277 aa, 1 stop

><MW: 30645, pI: 7.47, NX(S/T): 2

MNGFASLLRRNQFILLVLFLLQIQSLGLDIDSRPTAEVCATHTISPGPKGDDGEKGDPEEG
KHGKVGVMGPKGIKGELGDMGDQGNIGKTGPIGKKGDKGEKGLLGIPGEKGKAGTVCDGCRY
RKFFVQQLDISIARLKTSMKFVKNVIAGIRETEEFYIIVQEEKNYRESLTHCRIRGGMLAMP
KDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYMSTDNTPLQNYSNWNEGEPSPDPYGHEDC
VEMLSSGRWNDECHLTMYFVCEFIKKKK

Signal peptide:

amino acids 1-25

0097854-701601

FIGURE 38

GGTTCTATCGAATTGGAATTCGGCCACACTGGCCGGATCCTCTAGAGATCCCTCGACCTCGAC
CCAGCGCTCCGCTGCTCTCCGCCGCTGTGGAGTGGTGGGGGCTGGGTGGGAATGGGCGTGT
GCCAGCGCACGCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTTT
CGGAAGGGAGGATCAGGGATGTTTGCAGAGCGGCTGGAACAGACGGTGCCGATAGAGGAAGC
GGGCTCCATGGCTGCCCTCCTGCTGCTGCCCTGCTGCTGTTGCTACCGCTGCTGCTGCTGA
AGCTACACCTCTGGCGCGAGTTGCGCTGGCTTCCGGCGGACTTGGCCCTTTCGGGTGCGAGCT
CTGTGCTGCAAAAGGGCTTTCTGAGCTCGCGCCCTGGCCGCGGCTGCGCGCCAGCCCGAAGG
TCCCGAGGGGGGCTGCAAGCTGGCCCTGGCGCCTCGCGGAACCTGGCCCAGCAGCGCGCGCGC
ACACCTTTCTCATTCACGGCTCGCGCGCTTTAGCTACTCAGAGCGGAGCGCGAGAGTAAC
AGGGCTGCAACGCGCCTTCTACGTGCGCTAGGCTGGGACTGGGAGCCCGACGCGCGCGACAG
CGCGAGGGGAGCGCTGGAGAAGGCGAGCGGGCAGCGCCGGAGCCGAGATGTCAGCGCGCG
GAAGCGCGCGGAGTTTGCCGAGGGGACGGTGCCGCCAGAGGTGAGGAGCGCGCGCCCT
CTGTCACTGGAGCAACTGTGGCGCTGCTCCTCCCCGCTGGCCCAGAGTTTCTGTGGCTCTG
GTTCCGGGCTGGC CAAGGCGCGCTGCGCACTGCTTTGTGCGCCACCGCCTCGCGCGGGGCC
CCCTGTGCACTGCTCCGAGCTGCGGCGCGCGCGCTGGTGTGCGCGCAGAGTTTCTGTG
GAGTCCCTGGAGCCGAGACTGCCCGCCTGAGAGCCATGGGGCTCCACTGTGGGGTGCAAG
CCAGGAACCCACCTGCTGGAATTAGCGATTTGCTGGCTGAAGTGTCCGCTGAAGTGGATG
GGCCAGTGCCAGGATACCTCTCTCCCCCAGAGCATAACAGACACGTGCTGTACATCTTC
ACCTCTGGCACCCAGGGCCTCCCAAGGCTGCTCGGATCAGTCACTGAAGATCCTGCAATG
CCAGGGCTTCTATCAGCTGTGTGGTGTCCACCAGGAAGATGTGATCTACTCGCCCTCCAC
TCTACCACATGTCGGTTCCCTGCTGGGCATCTGGGCTGCATGGGCATTGGGGCCACAGTG
GTGCTGAAATCCAAAGTTCTCGGCTGGTCAAGTTCTGGGAAGATTGCCAGCAGCACAGGGTGAC
GGTGTTCAGTACATTGGGGAGCTGTGCCGATACCTTGTCAACAGACCCCGAGCAAGGCGAC
AACGTGCGCATAAAGGTCGCGCTGGCAGTGGGCAGCGGGCTGCGCCAGATACCTGGGAGCGT
TTTGTGCGCGCTTCCGGCCCTGCGAGTGTCTGGAGACATATGGACTGACAGAGGGCAACGT
GGCCACCATCAACTACAGGACAGCGGGCGCTGTGGGGCGTGCTTCTGGCTTTACAAGC
ATATCTTCCCTTCTCCTTGATTGCTATGATGTCAACACAGGAGAGCCAAATTCGGGACCCC
CAGGGGCGCTGATGGCCACATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCCGTAAGCCA
GCAGTCCCAATTCCTGGGCTATGCTGGCGGGCAGAGCTGGCCAGGGGAAGTTGCTAAAGG
ATGCTTCCGGCCTGGGATGTTTTCTTCAACACTGGGGACCTGCTGGTCTGCGATGACCAA
GGTTTTCTCCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAGAATGTGGC
CACAAACGAGGTGGCAGAGGTCTTCAGGGCCCTAGATTTCTTCAGGAGGTGAACGTCTATG
GAGTCACTGTGCAGGGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCC
CACGCTTTGGACCTTATGAGCTCTACACCCAGCTGTCTGAGAACTTGCCACCTTATGCCCCG
GCCCCGATTCCTCAGGCTCCAGGAGTCTTTGGCCACACAGAGACCTTCAAACAGCAGAAAG
TTCCGATGGCAAAATGAGGGCTTCGACCCAGCACCTGTCTGACCCACTGTACGTTCTGGAC
CAGCTGTAGGTGCTACTCTGCCCTTCACAACTGCCCGGTACAGCGCTCCTGGCAGGAAA
CCTTCGAATCTGAGAACCTCCACACCTGAGGCACCTGAGAGAGGAACCTGTGGGGTGGGGG
CCGTTGCAAGGTGACTGGGCTGTGAGGATCTTTTCTATACAGAACTGCGGTCACTATTTT
GTAATAAATGTAGCTGGAGCTGATCCAGCTGTCTGACCTAAAAAATAAATAAATAA
AAAAAATAAGGGCGCGCGACTCTAGAGTCGACCTGCGATAGGATTAACAGGGTAATAAGC
TTGGCCGCCATGGCCCAACTTGTTATTTCAG

0973564-101501

FIGURE 39

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50913

><subunit 1 of 1, 730 aa, 1 stop

><MW: 78644, pI: 7.65, NX(S/T): 2

MGVCQRTAPWKEKSQLERAALGFRRKGGSGMFASGWNQTVPIEEAGSMAALLLLPLLLLLPL
LLLKLHLWPQLRWLPADLAFVAVRALCKRALRARALAAAAADPEGPEGCSLAWRLAELAQQ
RAAHTFLIHGSRFRFSYSEAESNRARAFLRALGWDWGPDDGSDGEGSAGEGERAAPGAGD
AAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPEFLWLWFLAKAGLRTAFVPTAL
RRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSA
EVDGVPVPGYLSPPQSITDTCLYIFTSGETTGLPKAARISHLKILQCQGGFYQLCGVHQEDVIYL
ALPLYHMSGSLLGIVGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPP
SKAERGHKVR LAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINYTGORGAVGRASW
LYKHIFPFSILIRYDVTTEGPIRDPQGHCMATSPGEPGLLVAPVSQQSPFLGYAGGPBLAQK
LLKDVFRPGDVFFNTGDLVLCDDQGFLRFHVRTGDTFRWKGENVATTEVAEVFEALDFLQEV
NVYGVTVTPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPFYARPRFLRLQESLATTETFK
QQKVRMANEGFDPSTLSDPVLDQAVGAYLPLTTARYSALLAGNLR

Type II transmembrane domain:

amino acids 45-65

Other transmembrane domain:

amino acids 379-398

cAMP- and cGMP-dependent protein kinase phosphorylation site
starting at amino acid 136

CUB domain protein motif

amino acids 254-261

putative AMP-binding domain signature

amino acids 332-343

N-glycosylation sites

amino acids 37-40 and 483-486

00073564.10601

FIGURE 40

CCCTGTGTTAAGCTGAGGTTTCCCCTAGATCTCGTATATCCCCAACACATACCTCCACGCACA
CACATCCCCAAGAACCCTCGAGCTCACACCAACAGACACACGCGCGCATACACACTCGCTCTC
GCTTGTCCATCTCCTCCCGGGGAGCCGGCGCGCTCCACCTTTGCCGCACACTCCGGC
GAGCCGAGCCCGCAGCGCTCCAGGATTCTGCGGCTCGGAACTCGGATTGCAGCTCTGAACCC
CCATGGTGGTTTTTAAACACTTCCTTTCTCTCTCTCTCGTTTGTATTGCACCGTTTCCA
TCTGGGGGCTAGAGGAGCAAGGCAGCAGCCTTCCAGCCAGCCCTTGTGGCTTGCATCGT
CCATCTGGCTTATAAAAGTTTGTCTGAGCGCAGTCCAGAGGGCTGCGCTGCTCGCTCCCTCGG
CTGGCAGAAGGGGGTGACGCTGGGCAGCGGCAGGAGCGCGCTGCCCTTCTGCGGGCTTT
CGGCTTGAGGGGCAAGGTGAAGAGCGCACCGGCGGTGGGGTTTACCGAGCTGGATTGTATG
TTGCACCATGCTCTCTTGGATCGGGCTGTGATTCTTCCCTCTTGGGGCTGCTGCTCTCCC
TCCCGCGCGGGCGGATGTGAAGGCTCGGAGCTGCGGAGAGGTCCGCGAGGCGTACGGTGCC
AAGGGATTTCAGCTTGGCGGACATCCCTTACCAGGAGATCGCAGGGGAACACTTAAGAATCTG
TCCTCAGGAATATACATGCTGCACCAACAGAAATGGAAGACAAGTTAAGCCAACAAAGCAAAC
TCGAATTTGAAAACCTTGTGGAAGAGACAAGCCATTTTGTGCGCACCACTTTTGTGTCCAGG
CATAAAGAAATTTGACGAATTTTCCGAGAGCTCCTGGAGAATGCAGAAAAGTCACTAAATGA
TATGTTTGTACGACCTATGTCATGCTGTATCATGCAGAATTCAGAAGTCTTCCAGCCCTCT
TCACAGAGCTGAAAAGGTACTACACTGGGGTAATGTGAATCTGGAGGAATGCTCAATGAC
TTTGGGCTCGGCTCCTGGAACGGATGTTTTCAGCTGATAAACCTCAGTATCACTTCAGTGA
AGACTACCTGGAATGTGTGAGCAAATACACTGACCAGCTCAAGCCATTTGGAGACGTGCCCC
GGAAACTGAAGATTTCAGTTTACCGCGCCTTCATTGCTGCCAGGACCTTTGTCCAGGGGCTG
ACTGTGGGCGAGAAAGTTGCAAAACCGAGTTTCAAGGTGAGCCCAACCCAGGGGTGTATCCG
TGCCCTCATGAAGATGCTGTACTGCCATACGTGCGGGGCTTCCCATCTGTGAGGCCCTCGCA
ACAACTACTGCTCTCAACGTATGAAGGGCTGCTTGGCAAATCAGGCTGACCTCGACACAGAG
TGGAATCTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCGACTGGAGGGGCCATTCACAT
TGAGTCGGTTCATGACCCGATAGATGTCAAGATTCTGAAGCCATTATGAACATGCAAGAAA
ACAGCATGCAAGGTGTCTGCAAAGGTCTTTTCAGGGATGTGGTCAGCCCAACCTGCTCCAGCC
CTCAGATCTGCCCCGCTCAGCTCCTGAAAATTTAATAACGTTTCAGGCCCTACAATCCTGA
GGAAAGACCAACAACTGTGCAAGGCAACAGCTTGGACCGGCTGGTCACAGACATAAAGAGA
AATTGAAGCTCTCTAAAAAGGTCTGGTCAGCATTACCCTACACTATCTGCAAGGACGAGAGC
GTGACAGCGGGCAGCTCCAACGAGGAGGAATGCTGGAACGGGCACAGCAAAGCCAGATACTT
GCCTGAGATCATGAATGATGGGCTCACCACCCAGATCAACAATCCCGAGGTGGATGTGGACA
TCACTCGGCTGACACTTTCATCAGACAGCAGATTATGGCTCTCCCGTGTGATGACCAACAAA
CTAAAAAACGCCCTACAATGGCAATGATGTCAATTTCCAGGACACAAGTGTGAATCCAGTGG
CTCAGGGAGTGGCAGTGGGTGCATGGATGACGTGTGTCACACGGAGTTTGAATTTGTACCA
CAGAGGCCCCCGCAGTGGATCCCGACCGGAGAGAGGTGGACTCTTCTGAGCCAGCGTGGC
CACTCCCTGCTCTCCTGTCTCTACCTGCATTTGCTCTGGCATGACAGAGACTGTGCAGATA
ATCTTGGGTTTTTGGTCAGATGAACTGCATTTAGCTATCTGAATGGCCAATCACTTCTT
TTCTTACACTCTTGGACAATGGACCATGCCACAAAACCTTACCGTTTTCTATGAGAAGAGAG
CAGTAATGCAATCTGCCTCCCTTTTGTTTTCCAAAGAGTACCGGGTGCCAGACTGAACTG
CTTCCCTTTTCCCTCAGCTATCTGTGGGACCTTGTATTCTTGAAGAGAAATCTTATCAAA
ATTTTTCTGTACCAGGAGATTTCTTACCTTCATTGTCTTTATGCTGCAGAAGTAAAGGAAT
CTCAGTTGTGAGGGTTTTTTTTTCTCATTTAAAT

09973564.401601

FIGURE 41

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914

><subunit 1 of 1, 555 aa, 1 stop

><MW: 62736, pI: 5.36, NX(S/T): 0

MPSWIGAVILPLLGLLLSLPAGADVKARSCGEVRQAYGAKGFSLADIPYQEIAGEHLRICPQ
EYTCCTTEMEDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLENAESKSLNDF
VRTYGMLYMQNSEVFQDLFTELKRYYTGGNVNLEEMLNDFWARLLERMFQLINPQYHFSE
LECYSKYTDQLKPFQDVPRKLKIQVTRAFIAARTFVQGLTVGREVANRVSKVSPTPGCIRAL
MKMLYCPYCRGLPTVRPCNNYCLNVKMGCLANQADLDTAWNLFIDAMLLVAERLEGPFFNIES
VMDPIDVKISEAIMNMQENSMQVSAKVFQCGQPKPAPALRSARSAPENFNTRFRPYNPEER
PTTAAGTSLDRLVTDIKEKLKLSKKVWSALPYTICKDESVTAGTSNEEECWNGHSKARYLPE
IMNDGLTNQINNPEVDVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSG
SGSGCMDDVCPTEFEFVTTTEAPAVDPDRREVDSSAAQRGHSLLSWSLTCIVLALQRLCR

Signal peptide:

amino acids 1-23

007361.01602

FIGURE 42A

CGGACGCGTGGGCGGACGCGTGGGCAAAGAAGCTCGGAGTGCCAAAGCTAAATAAGTTAGCTGAGAAAAACGACG
 CAGTTTGCAGCGCCTTCGCGCGGGTGCGCCAACTACGCAAGAAGCAAGCGGGCTCCGCGCGGACGCGCCGCGGGG
 TAGGGACCGCGCTTTGGCCTTCAGGCTCCCTAGCAGCGGGGAAAGGAATTGCTGCCCGGAGTTTTCGCGGAGGT
 GGAGGGAGATCAGGAAACGGCTTCTTCTCACTTCGCGCGCTGGTGAAGTTCGCGGAGAGATTGGCAAACCGCTTAGG
 AAAGGACTGGGAAAAATAGCCCTGGGAAAGTGGAGAAGGTGATCAGGAGGCGCGTCCACTACGCGAGTTTATCTG
 TCTGATCAGAGCCAGCGCGACGCGTCCACTTCGCAAGTTCTTCCAGGTGTGGGGACCGCAGGACAGACGCGCCGA
 TCCGCGCGCCCTCGTACCAGCACTCCAGGAGAGTCAGCCTCGCTCCCAACGTCGAGGGCGCTCTGGCCACGA
 AAAGTTCCTTCCACTGTGATTCTCAATTCCTGTGTGGTTTTTCTCAGGAAGATTTCGGGTGGAGATATTA
 ACTTTTTCTTTTTTTTTTCTTGGTGAAGCTGCTCAGGGAGGGGGAGGAGGAGGAGAAAGTGAATGTGC
 TGGAGAAGAGCGAGCCCTCCTGTGTTCTCCGAGTCCCATCATAAGCCATCACTTCTGGAAGATTAAAGTTGT
 CGGACATGGTGACAGCTGAGAGGAGGAGGATTTCCTGCCAGGTGGAGAGTCTTCAACGCTGTTGGGTGCATG
 TGTGCGCCGCGAGCGCGCGGGCGCGTGGTTCCCGCGTGGAGTCTCACTGGGACCTGAGTGAATGCTCCCA
 GGGGCTGTGCGGGGCATCCGCTCCGCGCTTCTCCACAGGCGCTGTGTCTGCTCCGGAAAGATTGGCAATGGGG
 CGCTGGCAGGATTCTGGATCCTCTGCTCCTCACTTATGGTTACCTGTCTGGGGCCAGGCTTAGAAGAGGAGG
 AAGAAGGGGCTTACTAGCTCAAGCTGGAGAGAACTAGAGCCAGCACACTTCCACCTCCAGCGCCATCTCA
 TTTTCATCTAGCGGATGATCAGGGATTAGAGATGTGGGTTACCAAGGATCTGAGATTAAAAACACCTACTCTTG
 ACAAGCTCGCTCCGCAAGGAGTTAAACTGGAGAACTACTATGTCCAGCCTATTGTGACACCATCCAGGAGTCAGT
 TTATTACTGAAAGTATCAGATACACACCGACTTCAACATTCTATCATAAGACCTACCCAAACCCACTGTTTAC
 CTCTGGACAATGCCACCTACCTCAGAAACTGAAGGAGGTGGATATTCAACGCATATGGTCGGAATATGGCACT
 TGGGTTTTTAACAGAAAAGATGCATGCCACCAGAAAGAGGATTGATACCTTTTTTGGTTCCTTTTGGGAAAGT
 GGGATTACTATACACATAAATGACAGTCTCTGGGATGTGGTCTATGACTTGTATGAAAACGACAAATGCTG
 CCTGGGACTATGACAATGGCATATACTCCACACAGATGTCACTCAGAGAGTACAGCAAATCTTAGCTTCCGATA
 ACCCCACAAAGCCTATATTTTTATATATCTGCTATCAAGCTGTTCATTACCACTGCAAGCTCCTGGCAGGTATT
 TCGAACACTACCGATCCATTATCAACATAAAGAGGAGAAGATATGCTGCCATTGTTCTGCTTAGATGAAGCAA
 TCAACAACGTGACATTGGCTCTAAGACTTATGGTTTCTATAAACAAGCATTATCATTTACTCTTCAGATAATG
 GTGCCAGCCTACCGCAGGAGGGAGTAACTGGCTCTCAGAGGTAGCAAAGGAACATATTGGGAAGGAGGATCC
 GGGCTGTAGGCTTTGTGCTAGCCCACTTCTGAAAAACAAGGGAACAGTGTGTAAAGAACTTGTGCACATCACTG
 ACTGGTACCCCACTCTCATTTCACTGGCTGAAGGACAGATTGATGAGGACATTCAACTAGATGGCTATGATATCT
 GGGAGACCATAAGTGAGGGTCTTCGCTCACCCGAGTAGATATTTTGCAATAACATTGACCCCTATACACCAAGC
 AAAAAATGGCTCTCGGCAGCAGGCTTAGGGATCTGGAACATCGCAATCCAGTCAGCCATCAGAGTGCAGCACTG
 GAAATGTCTTACAGGAAATCCTGGCTACAGCGACTGGTCCCCCTCAGTCTTTAGCAACCTGGGACCGGAACG
 GTGGCAATGAACGGATCACCTTGTCACTGGCAAAAGTGTATGGCTTTTCAACATCAACGCGACCCATATGA
 GAGGGTGGACCTATCTAACAGGTATCCAGGAATCTGAGAGAAGCTCTACGAGGCTCTCAAGTTCAACAAAAC
 TGCACTGCGGTGAGTATCCCCCAAAGACCCAGAAGTAACCTTAGGCTCAATGGAGGGGTCTGGGGACCATG
 GTATAAAGAGGAACCAAGAAAAAGAACCAAGCAAAATCAGGCTGAGAAAAAGCAAAAGAAAAAGCAAAAAA
 GAAGAAGAAACAGCAGAAAGCAGTCTCAGGTAAACAGCAAAATTTGGCTCGATAATATCGCTGGCCTAAGCGTCA
 GGCTGTGTTTTCATGCTGTGCCACTCCAGAGACTTCTGCCACCTGGCCGCCCACTGAAAACTGCTCTGCTCAGTG
 CCAAGGTGCTACTCTTGCAAGCCACTTAGAGAGAGTGGAGATGTTTATTTCTCTGCTCTTTAGAAAAAGCTG
 GTGAGTCTCGAGTTTCCAGTCTGTGCTTCACTGACCAAAACACTGCTTTGAATTATAGGAGGAGAACATA
 ACCTACCATCCGCAAGCATGCTAATTTGATGGAAGTTACAGGGTAGCATGATTAAAGCTACCTTTGATAAATTAC

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AGTCAAAGATTGTGTCACTCAAAGGCCCTGAAGAATATATTTTCTTGGTGAAATTTTGTATGTCTGTCAATGA
CACTTGGGTTTTTAAATTAATCTATTTTATATATATAAATATATGTTCTTTCTCTGTGAAAGCTGTTTTCT
CACATGTGAACAGCTTGTCACTCTAATCTTTTACCATGCGTGGAGGAATGGCAAATAAGAAATGTTTGGACACACTGCC
ACAAATGAATGTAACATTATTTCTAAACCTTTACTAGAAGACAACTTCGATATAAAAAACCTAAATTTATTTTACA
GAAAAATATTTTGTGTTTTTATAAAAAAGTATGCAAACTGACTTTTTATTTTATTTCTCGCATCACTATAGAAGA
ATTTTATTTCAATTTCTTCAAAATATCAAGCACTGTAATACATATAAATTAATGTAATCTGTGTGAATTGAGACTA
TAAAAAACCATTCATTCAGAAAACTTTATAATCTGTCATTGTTCAATCAAGATTTTGAATGTAATAAGATGAATATAT
ATTACTTGGAAATTCATGTGTTGTGCGAGGTGAGACAACTTTTATGTTTCTATCAATAAATCTTATGTATCTT
AATATATAAATGATTTTACTTTATGGCACAAGAAATTTACTGTGGCTTTCTTGATCTTAACCTCTAGCTAAAAAT
GTATCATTTGGTCTTAAAAAATAAAATCTTTACTAATAGGCAATTGAAGGAATGGTTTGTCAACAAACCAAGTAA
TATAATATGATTTTACAGATAGATGCTTCCCTTGGCTTGAATGACATGGAGAAAGATTTTCCCATTAATATAACTAA
TTTATATATTTAGGTTGGTGCAAAACTAGTGTGCGGTTTTTCCCATTAAGAGTAATAAACCCTTCTCTTATACAAAGT
GGACATGTGGGGAGATACAGAGAATGAAGATACGGAATCTGCTCGTGGAGTAGGTAACCTTACTGTCTGAAAACCCC
ACATGCAAAAGCTCATGAGGAGAAATAAGGAGATATATCAGTAATGAAGTTTATCTGGGTCTCAATGAGCATA
GATTGGTGTGGAATCCTGTAGACCTTGGTGTCTTCTTGAAGTGCCCTCTCCTAATGCAGAGGCCCTTGAAGCTTAC
AGTATACACTTGAAAAGCTCACAGATACCTAGAATATATGATCTTGAAGTTATAACTGTGATCTGAAAATGTGTGT
GGTGGTATGCAGACATACCATTAAATACATTACATCAGAGCTCAAGGACGTGTGATATAATCCATTTATATCAC
AAGCTCAAGAGCTGTGATATAATCATTATATCAGCAGTACAGATTTCTGAAAATGATATAAGAAATCTATAAT
CTAGTACTGAAATTAATAAATGGGTAAAGATGATTTAAATGATTTTAATTTAAACATTTTATTTCTAGAATATAT
GGCTCCATTTTATTTATAGTGTAAAGTTGTAATTTCTTAAAGTTTGTGTTTGTGCGACAGTATCTTTTAAATGAG
TCTTAAAAAATAAGGCATATGTTCTATGTTTAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA
TCTTAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA

FIGURE 43

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296
><subunit 1 of 1, 515 aa, 1 stop
><MW: 56885, pI: 6.49, NX(S/T): 5
MAPRGCAGHPPPPSPQACVCPGKMLAMGALAGFWILCLLTYGYLSWGQALEEEEEEGALLAQA
GEKLEPSTTSTSQPHLIFILADDQGFRDVGYPHGSEIKTPTLDKLAAGVKLENYYVQPICTP
SRSQFITGKYQIHTGLQHSIIIRPTQPNCLPLDNATLPQKLKEVGYSTHMGVKGWHLGFNRKEC
MPTRRGFDTFFGSLLGSGDYTHYKCDSPGMCGYDLYENDNAAWDYDNGIYSTQMYTQRVQQ
ILASHNPTKPIFLYTAQAVHSPLQAPGRYFEHYRSIININRRRYAAMLSCLEAINNVTLA
LKTGYGFYNNNSIIYSSDNGGQPTAGGSNWPLRGSKGTYWEGGIRAVGFVHSPLLKNKGTVCCK
ELVHITDWPYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSRPRVDILHNIDPYTPRQKMAPG
QQAMGSGTLQSSQPSECSTGNCLEILATATGSPLSLSTWDRGTGTMNGSPCQLAKVYVGS
TSQPTHMRGWYTLTGIOES

Important Features:

Signal Peptide:

amino acids 1-37

Sulfatases signature 1.

amino acids 120-132

Sulfatases signature 2.

amino acids 168-177

Tyrosine kinase phosphorylation site.

amino acids 163-169

N-glycosylation sites.

amino acids 157-160, 306-309 and 318-321

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FIGURE 44

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGGCGGC
 TTAGCTGCTACGGGGTCCGGCCGGCGCCCTCCCGAGGGGGGCTCAGGAGGAGGAAGGAGGAC
 CCGTGCAGAGAATGCGCTTGCCTTGGAGCCTTGCCTCCCGCTGCTGCTCTCCTGGGTGGCAG
 GTGGTTTCGGGAACGCGGCCAGTGAAGGCATCACGGGTGTGTTAGCATCGGCACGTGAGCCT
 GGGGTCTGTCACTATGGAATAAACTGGCCTGCTCTACGGCTGGAGAAGAAAAGCAAGGAGG
 AGTCTGTGAAGCTACATGCGAACCTGGATGTAAGTTTGGTGAAGTGCCTGGGACCAACAAAT
 GCAGATGCTTTCCAGGATACACCGGAAAACTGCAGTCAAGATGTGAATGAGTGTGGAATG
 AAACCCCGGCCATGCCAACACAGATGTGTGAATACACAGGAAGCTACAAGTGTCTTTGCTCT
 CAGTGGCCACATGCTCATGCCAGATGTACGTGTGTGAATCTTAGGACATGTGCCATGATAA
 ACTGTCACTACAGCTGTGAAGACACAGAAGAAGGGCCACAGTGCTGTGTCCATCCTCAGGA
 CTCGCGCTGGCCCCAAATGGAAGAGACTGTCTAGATATTGATGAATGTGCCTCTGGTAAAGT
 CATCTGTCCCTACAATCGAAGATGTGTGAACACATTTGGAAGCTACTACTGCAATGTGACA
 TTGGTTTCGAACTGCAATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGTACT
 ATGGATAGCCATACGTGCAGCCACCATGCCAATTGCTTCAATACCCAGGGTCTTCAAGTG
 TAAATGCAAGCAGGGATATAAAGGCAATGGACTTCGGTGTCTGCTATCCCTGAAAAATTCTG
 TGAAGGAAGTCTCAGAGCACCTGGTACCATCAAAGACAGAATCAAGAAGTTGCTTGCTCAC
 AAAAAACAGCATGAAAAAGAAGGCAAAAAATTAAAAATGTTACCCAGAACCCACCAGGACTCC
 TACCCCTAAGGTGAACCTTGACGCCCTTCAACTATGAAGAGATAGTTTCCAGAGGCGGGAAC
 CTCTATGGAGGTAAAAAAGGGAATGAAGAGAAATGAAGAGGGGCTTGAGGATGAGAAAAAGAG
 AAGAGAAGCCCTGAAGAAATGACATAGAGGAGCGAAGCCTGCGAGGAGATGTGTTTTCCCT
 AAGGTGAATGAAGCAGGTGAATTCGGCCTGATTCTGGTCCAAAGGAAGCGCTAACTTCCAA
 ACTGGAACATAAAGATTAAATATCTCGGTTGACTGCAGCTTCAATCATGGGATCTGTGACT
 GGAACACAGGATAGAGAAGATGATTTTGAAGTGAATCCTGCTGATCGAGATAATGCTATTGGC
 TTCTATATGGCAGTTCCGGCCTTGGCAGGTCAAGAAGAGACATTGGCCGATTGAAACTTCT
 CCTACCTGACCTGCAACCCCAAAGCAACTTCTGTTTGGCTCTTTGATTACCGGCTGGCCGGAG
 ACAAGTTCGGGAACTTCGAGTGTGTGTGAAAAACAGTAACATGCCCTGGCATGGGAGAAG
 ACCACGAGTGAGGATGAAAAGTGAAGACAGGGAAAAATTCAGTTGTATCAAGGAACTGATGC
 TACCAAAAGCATCATTTTTGAAGCAGAACTGGGCAAGGGCAAAACCGCGAATCGCAGTGG
 ATGGCGTCTTGCTTGTTTCAGGCTTATGTCCAGATAGCCTTTATCTGTGGATGACTGAATG
 TTACTATCTTTATATTTGACTTTGTATGTGAGTTCCCTGGTTTTTTTGATATTGCATCATAG
 GACCTCTGGCATTTTAGAATTACTAGCTGAAAAATTTGTAATGTACCAACAGAAAAATTATTG
 TAAGATGCCTTTCTGTATTAAGATATGCCAATATTTGCTTTAAATATCATATCACTGTATCT
 TCTCAGTCATTCTGAATCTTTCCNCATTATATTAAAAATNTGGAANGTCAGTTTATCTC
 CCTCTCCTGATATACTGATTGTATANGTANGTTGATGNGCTTCTCTCTACAACATTCTTA
 GAAAAATAGAAAAAAGCACAGAGAAATGTTTAACTGTTTGACTCTTATGATACTTCTTGA
 AACTATGACATCAAAGATAGACTTTTGCTTAAGTGGCTTAGCTGGGCTTTTCATAGCCAAAC
 TTGTATATTTAATCTTTGTAATAATAA

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGGCGGC

FIGURE 45

MPLPWSLALPLLLSWVAGGFGNAASARHHGLLASARQPGVCHYGTKLACCYGWRRNSKGVCE
ATCEPGCKFGECVGNKCRCFPGYTGTKCSQDVNECGMKPRPCQHRCVNTHGSKYKCFCLSGH
MLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAPNGRDCLDIDECASGKVICP
YNRCVNTFGSYYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKCK
QGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAHKNSMKKKAKIKNVTPEPTRTPTPK
VNLQPFNYEEIVSRGGNSHGGKKGNEEK

Signal peptide:

amino acids 1-21

EGF-like domain cysteine pattern signature.

amino acids 80-91

Calcium-binding EGF-like domains

amino acids 103-124, 230-251 and 185-206

FIGURE 46

GGGAGCTGCTGCTGTGGCTGCTGGTGTGTGCGCGTCTCTCTGCTCTTGGTGCAGCTGCTG
CGCTTCTTGAGGGGTGACGGCGACCTGACGCTACTATGGGCCGAGTGGCAGGGACGACGCC
AGAATGGGAGCTGACTGATATGGTGGTGTGGGTGACTGGAGCCTCGAGTGGAAATTGGTGAGG
AGCTGGCTTACCAGTTGTCTAAACTAGGAGTTTCTCTTGTGCTGTGAGCCAGAAGAGTGTCAT
GAGCTGGAAAGGGTGAAAAGAAGATGCCTAGAGAATGGCAATTTAAAAGAAAAGATATACT
TGTTTTGGCCCTTGACCTGACCGACACTGGTTCCCATGAAGCGGCTACCAAAGCTGTTCTCC
AGGAGTTTGGTAGAATCGACATTCTGGTCAACAATGGTGGAATGTCCAGCGTTCTCTGTGC
ATGGATACCAGCTTGGATGTCTACAGAAAGCTAATAGAGCTTAACTACTTAGGGACGGTGTC
CTTGACAAAATGTGTTCTGCCTCACATGATCGAGAGGAAGCAAGGAAAGATTGTTACTGTGA
ATAGCATCCTGGGTATCATATCTGTACCTCTTTCCATGGATACTGTGCTAGCAAGCATGCT
CTCGGGGTTTTTTAATGGCCTTCGAACAGAACTTGCCACATACCCAGGTATAATAGTTTC
TAACATTTGCCCAGGACCTGTGCAATCAAATATTTGGGAGAATTCCCTAGCTGGAGAAGTCA
CAAAGACTATAGGCAATAATGGAGACCAGTCCCACAAGATGACAACCAAGTCGTTGTGTGCGG
CTGATGTTAATCAGCATGGCCAATGATTTGAAAGAAGTTTGGATCTCAGAACCAACCTTTCTT
GTTAGTAACATATTTGTGGCAATACATGCCAACCTGGGCCTGGTGGATAACCAACAAGATGG
GGAAGAAAAGGATTGAGAAGCTTTAAGAGTGGTGTGGATGCAGACTCTTCTTATTTTAAAATC
TTTAAGACAAAACATTGACTGAAAAGAGCACCTGTACTTTTCAAGCCACTGGAGGGAGAAATG
GAAAACATGAAAACAGCAATCTTCTTATGCTTCTGAATAATCAAAGACTAATTTGTGATTTT
ACTTTTTAATAGATATGACTTTGCTTCCAACATGGAATGAAATAAAAAATAAATAAAAAG
ATTGCCATGAATCTTGCAAAA

097554.101601

FIGURE 47

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA36343
><subunit 1 of 1, 289 aa, 1 stop
><MW: 32268, pI: 9.21, NX(S/T): 0
MVVVVTGASSGIGEELAYQLSKLGVSLVLSARRVHELERVKRRCLEENGLKEKDILVLPLDL
TDTGSHEAATKAVLQEFGRIDILVNNGGMSQSRSLCMTSLDVYRKLIELNYLGTVSLTKCVL
PHMIERKQGGKIVTVNSILGIISVPLSIGYCASKHALRGFFNGLRTELATYPGIIIVSNICPGP
VQSNIVENSLAGEVTCTIGNNGDQSHKMTTSRCVRLMLISMANDLKEVWISEQPFLLVTYLW
QYMPTWAWWITNKMGGKKRIENFKSGVDADSSYFKIFKTKHD

Important Features:

Signal Peptide:

amino acids 1-31

Transmembrane domain:

amino acids 136-157

Tyrosine kinase phosphorylation site.

106-113 and 107-114

Homologous region to Short-chain alcohol dehydrogenase

amino acids 80-90, 131-168, 1-13 and 176-185

FIGURE 48

GGGACGTGGGCACCGCCATCAGCTGTTTCGCGCTCTTCTCCTCCAGGTGGGGCAGGGGTTTC
GGGCTGGTGGAGCATGTGCTGGGACAGGACAGCATCCTCAATCAATCCAACAGCATATTTCGG
TTGCATCTTCTACACACTACAGCTATTGTTAGGTTGCTGCGGACACGCTGGGCCTCTGTCC
TGATGCTGCTGAGCTCCTCGTGTCTCTCGCTGGTTCTGTCTACCTGGCCTGGATCCTGTTTC
TTCGTGCTCTATGATTTCGCATTGTTTGTATCACCACCTATGCTATCAACGTGAGCCTGAT
GTGGCTCAGTTTCCGGAAGGTTCCAAGAACCCAGGGCAAGGCTAAGAGGCACTGAGCCCTCA
ACCCAGCCAGGCTGACCTCATCTGCTTTGCTTTGGTCTTCAAGCCGCTCAGCGTGCTCTGTG
GACAGCGTGGCCCGCGGCCCGCCAGCCTCAGGAGGGCAACACAGTCCCTGGCGAGTGGCCCC
TGGCAGGCCAGTGTGAGGAGGCAAGGAGCCACATCTGCAGCGGCTCCTGGTGGCAGACAC
CTGGGTCTCTACCTGCTGCCACTGCTTTGAAAGGGCAGCAGCAACAGAACTGAATTCTGGT
CAGTGGTCTCTGGGTTCTCTGCAGCGTGAGGGACTCAGCCCTGGGGCCGAAGAGGTGGGGGTG
GCTGCCCTGCAGTGGCCAGGGCCTATAACCACTACAGCCAGGGCTCAGACCTGGCCCTGCT
GCAGCTCGCCACCCACGACCCACACACCCCTCTGCCTGCCAGCCCGCCCATCGCTTCC
CCTTTGGAGCCTCCTGCTGGGGCACTGGCTGGGATCAGGACACAGTGATGCTCCTGGGACC
CTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAACCTGTATCTACAACCACT
GCACCAAGCACACCTGTCCAACCGGCCCGGCTGGGATGCTATGTGGGGGCCCCAGCCTG
GGGTGCAGGGCCCTGTGAGGAGATTCGGGGGCCCTGTGCTGTGCTCGAGCCTGACGGA
CACTGGGTTGAGGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCAGGAGGACGCTCCTGT
GCTGCTGACCAACACAGCTGCTCACAGTTCTCTGGCTGCAGGCTCGAGTTGAGGGGGCAGCTT
TCTTGGCCAGAGCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGA
TCCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCCTCCCATGGCCCTGGGAGGCCAGGCT
GATGCACCAAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGCGGTGCTAACTG
CTGCCCACTGCTTCATTTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACAGA
CCGGAGGAGTGGGGCCTGAAGCAGCTCATCTGCACTGGAGCCTACACCAACCTGAGGGGGG
CTACGACATGGCCCTCCTGCTGCTGGCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCC
TCTGCCTGCCCTATCCTGACCACCACTGCCTGATGGGGAGCGTGGCTGGGTTCTGGGACGG
GCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTACCCCTCCTGGGGCCTAG
GGCCTGCAGCCGGCTGCATGCACTCCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGG
TGTGTACCACTGCTGTGGGTGAGCTGCCAGCTGTGAGGGCCTGTCTGGGGCACCCTGGTG
CATGAGGTGAGGGGCACATGGTTCTGGCCGGGCTGCACAGCTTCGGAGATGCTTGCCAAGG
CCCCGCCAGGCCGGCGGTCTTCACCGCCTCCTGCTATGAGGACTGGGTGAGCAGTTTGG
ACTGCGAGGTCTACTTCCGCGAGGAACAGAGCCGAGGCTGAGCCTGGAAGCTGCTGGCC
AACATAAGCCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTCTCAGGACAAGAGAATGC
AGGCAGGCCAAATGGCATTACTGCCCTGTCTCTCCCAACCTGTGATGTGTGATTCCAGGCAC
CAGGCGAGGCCCAGAACGCCAGCAGCTGTGGGAAGGAACCTGCCTGGGGCCACAGGTGCCCA
CTCCCCACCTGCGAGGACAGGGGTCTCTGTGGACACTCCCAACCCAACTCTGCTACCAAGC
AGGCTCTCAGCTTTCTCTCTCTCTTACTCTTTTACAGTACAATCACGCCAGCCAGTGTGTT
TGAAATTTCTTTTTTTGGGGGGCAGCAGTTTTCTTTTTTAAACTTAAATAAATTTGTAC
AAAAATAAA

09978564.101601

FIGURE 49

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40571

MLLSSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGNTV
PGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGA
EEVGVAALQLPRAYNHYSQGSDDLALLQLAHPHTHTPLCLPQPAHRFPFGASCWATGWDQDTS
DAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDGGGPVLC
LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAFLAQS PETPEMSDEDS
CVACGSLRTAGPQAGAPSPWPWEARLMHQQLACGGALVSEEAVLTAACHFIGRQAPEEWSV
GLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLDPDGERG
WVLGRARPGAGISSLQTVPTLLGPRACSR LH AAPGGDGSPI LPMVCTSAVGELPSCEGLS
GAPLVHEVRGTWFLAGLHSFGDACQGPAPPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEF
GSCLANISQPTSC

Important features:

Signal peptide:

amino acids 1-15

Homologous region to Serine proteases, trypsin family

amino acids 79-95, 343-359 and 237-247

N-glycosylation sites.

amino acids 37-40 and 564-567

Kringle domains

amino acids 79-96, 343-360 and 235-247

FIGURE 50

CGGGCCGCCCGGCCCGCCCATTCGGGCCGGGCCTCGCTGCGGCGGCGACTGAGCCAGGCTGG
 GCCGCGTCCCTGAGTCCAGAGTCCGCGCGCGCGCGCAGGGGCAGCCTTCCACCACGGGGAG
 CCCAGCTGTACAGCCGCTCACAGGAAGATGCTGCGTCCGCGGGGCAGCCCTGGCATGGGTGT
 GCATGTGGGTGCAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCCAGG
 TCCTTGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCTGTGCTGCTCCTTCTCC
 CCTGAGCCTGGCTTACGCTGGCACAGCTCAACCTCATCTGGCAGCTGACAGATACCAAACA
 GCTGGTGCACAGCTTTGTCTGAGGGCCAGGACCAGGGCAGCGCCTATGCCAACCCGCACGGCCC
 TCTTCCCGGACCTGTCTGGCACAGGGCAACGCATCCCTGAGGCTGCAGCGCGTGCCTGTGGCG
 GACGAGGGCAGCTTCACTGTCTTCTGTAGCATCCGGGATTTCCGCAGCGCTGCCGTGAGCCT
 GCAGTGGCCGCTCCCTACTCGAAGCCAGCATGACCCTGGAGCCCAACAAGGACCTGCGGC
 CAGGGGACACGCTGACCATACGCTGTCCAGTACCAGGGCTACCCCTGAGGCTGAGGTGTTT
 TGGCAGGATGGGCAGGGTGTGCCCTGACTGGCAACGTGACCAGTGCAGATGGCCAAACGA
 GCAGGGCTGTGTTGATGTGCACAGCGTCTTCTCGGGTGGTGTCTGGGTGCGAATGGCACCTACA
 GCTGCCCTGGTGCACAACCCCGTGTGCAGCAGGATGCGCACRGCTCTGTCAACATCACAGGG
 CAGCCTATGACATTTCCCCCAGAGGCCCTGTGGGTGACCGTGGGGCTGTCTGTCTGTCTCAT
 TGCACTGCTGGTGGCCCTGGCTTTCTGTGTCTGGAGAAAGATCAAACAGAGCTGTGAGGAGG
 AGAATGCAGGAGCTGAGGACCAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCT
 CTGAAACACTCTGACAGCAAAGAAGATGATGGACAAGAAATAGCCTGACCATGAGGACCAGG
 GAGCTGTACCCCTCCCTACAGCTCCTACCCCTCTGGCTGCAATGGGGCTGCACTGTGAGCCC
 TGCCCCAACAGATGCATCCTGTCTGTGACAGGTGGGCTCCTTCTCCAAAGGATGCGATACAC
 AGACCACTGTGCAGCCTTATTTCTCCAATGGACATGATTCCCAAGTCATCCTGTGCCTTTT
 TTCTTATAGACACAATGAACAGACCACCCACAACCTTAGTTCTCTAAGTCATCCTGCCTGTCT
 GCCTTATTTACAGTACATACATTTCTTAGGGACACAGTACACTGACCACATCACCACCCCTC
 TTCTTCCAGTGCTGCGTGGACCATCTGGCTGCCCTTTTTTCTCCAAAAGATGCAATATTGAGA
 CTGACTGACCCCTTGCTTATTTACACCAAAGACACGATGCATAGTCACCCCGGCCTTGTTC
 TCCAATGGCCGTGATACACTAGTGATCATGTTGAGCCCTGCTTCCACCTGCATAGAATCTTT
 TCTTCTCAGACAGGGACAGTGCGCCCTCAACATCTCTGGAGTCTAGAAGCTGTTTCTCTTC
 CCTCCTTCTCCTCCCTGCCCAAGTGAAGACAGGGCAGGGCCAGGAATGCTTTGGGGACACCG
 AGGGGACTGCCCCCCACCCCCACCATGGTGTCTATTCTGGGGCTGGGGCAGTCTTTTCTGGC
 TTGGCTCTGGCCAGCTCCTGGCCTCTGGTAGAGTGAGACTTCAGACGTTCTGATGCTTCCG
 GATGTCTCTCTCCTGCCCCAGGAATGGAAGATGTGAGGACTTCTAATTTAAATGTGGGAC
 TCGGAGGGATTGTAATACTGGGGGTATATTTGGGGAAAATAAATGTCTTTGTAAAAAAA
 AAAAAAAAAAAAAA

09978564.101601

FIGURE 51

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386
><subunit 1 of 1, 316 aa, 1 stop, 1 unknown
><MW: -1, pI: 4.62, NX(S/T): 4
MLRRRGSPGMGVHVGAAALGALWFCLTGALEVQVPEDPVVALVGTDATLCCSFSPGPGFSLAQ
LNLIIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLLAQGNASLRLQRVVRVADEGSFTCFV
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDQGQGVPL
TGNVTTSQMANEQGLFDVHSLRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTFPPEA
LWVTVGLSVCLIALLLVALAFVCWRKIKQSCEENAGAEDQDGEGETALQPLKHSDSKED
DGQEIA

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 251-270

N-glycosylation site.

amino acids 91-94, 104-107, 189-192 and 215-218

Homologous region to Immunoglobulins and MHC

amino acids 217-234

007064-10001

FIGURE 52

TTCTGTGACCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCTTCTAAGAAGGGGAGTC
CTGAACCTTGCTCTGAAGCCCTTGCCGTAAGCCTTGAACCTACGTTCTTAAATCTATGAAGTCG
AGGGACCTTTTCGCTGCTTTTGTAGGGACTTCTTTCCCTTGCTTCAGCAACATGAGGCCTTTTCT
TGTGGAACGCGGTCTTGACTCTGTTCTGCTACTTCTTTGATTGGGGCTTTGATCCCTGAACCA
GAAGTGAAGAATTGAAGTTCTCCAGAAGCCATTTCATCTGCCATCGCAAGACCAAGGAGGGGA
TTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAAGGACGGCTCCTTATTTCACCTCCATC
ACAAACATAACAATGGTCTAGCCCATTTGGTTTACCCCTGGGCATCCTGGAGGCTCTCAAGGT
TGGGACCAGGGCTTGAAGGAATGTGTGTAGGAGAGAAGAGAAAGCTCATCATCTCTCTCG
TCTGGGCTATGGAAGAAGAGGAAAAGGTAAAATCCCCCAGAAAAGTACACTGATATTTAATA
TTGATCTCCTGGAGATTGCAAAATGGACCAAGATCCCATGAATCATTTCCAAGAAATGGATCTT
AATGATGACTGGAACCTCTCTAAGATGAGGTTAAAGCATATTTAAAGAGGAGGTTTGA
ACATGTTGCCGTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTGATAAAG
AAGATGAAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAACACGATGAGTTA
TAGAGATACATCTACCCTTTTAAATAGCACTCATCTTTCAAGAGAGGGCAGTCATCTTTAA
AGAACATTTTATTTTATACAATGTTCTTTCTTGCTTTGTTTTTATTTTATATATTTTTT
CTGACTCCTATTTTAAAGAACCCTTAGGTTTCTAAGTACCCATTTCTTTCTGATAAGTTATT
GGGAAGAAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTCTACTTTCACAG
ATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAATGTTGCAACTGGGAATATACC
ACGACATGAGACCGAGTTATAGCACAAATTAGCACCCATATATTTCTGCTTCCCTCTATTTTCT
TCCAAGTTAGAGGTCAACATTTGAAAAGCCTTTTGCAATAGCCCAGGCTTGCTATTTTCAT
GTTATAATGAATAGTTTATGTGTAAGTCTGAGTCTCTGCTTGAGGACCAAGAGAAAA
TGGTTGTTGGACCTGACTTGTGTTAATGGCTACTGCTTTACTAAGGAGATGTGCAATGTCTGAAG
TTAGAAAACAGGTTAATAGCCAGGCATGTTGGCTCATGCTGTAATCCAGCACTTTGGGAG
GCTGAGGCGGGCGGATCACCTGAGGTTGGGAGTTCGAGACCAGCCTGACCAACACGGAGAAA
CCCTATCTCTACTAAAAATACAAAGTAGCCCGGCGTGGTGTATGCGTGCTGTAATCCAGCT
ACCCAGGAAGGCTGAGGCGGCAGAAATCACTTGAAACCGAGGCCGAGGTTGCGGTAAGCCGAG
ATCACCTNAGCCTGGACACTCTGTCTCGAAAAAAGAAAAAGAACACGGTTAATACCATATNA
ATATGTATGCATTGAGACATGTACCTAGGACTTAAGCTGATGAAGCTTGGCTCCTAGTGAT
TGGTGGCCCTATTATGATAAAATAGGACAAATCATTTAAGTGTGAGTTTCTTTGTAATAAAATG
TATCAATATGTTATAGATGAGGTAGAAAAGTTATATTTATATTTCAATATTTACTTCTTAAGGC
TAGCGGAATATCCTTCTGGTTCTTTAATGGGTAGTCTATAGTATATTATACTACAATAACA
TTGTATCATAAAGATAAAGTAGTAAACCAAGTCTACATTTTCCCATTTCTGTCTCATCAAAAAC
TGAAGTTAGCTGGGTGTGGTGGCTCATGCTGTAATCCAGCACCTTTGGGGGCCAAGGAGGG
TGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAACCTTGTCTCTA
CTAAAAATACAAAAATTAGCCAGGCGTGGTGGTGCACACCTGTAGTCCAGCTACTCGGGAG
GCTGAGACAGGAGATTTGCTTGAACCCGGGAGGCGGAGGTTGCACTGAGCCAAAGATTGTGCC
ACTGCATCCAGCTGGGTGACAGAGCAAGACTCCCATCTCAAAAAAAGAAAGAGCAGA
CCTACAGCAGCTACTATTGAATAAATACCTATCCTGGATTTT

FIGURE 53

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44194
><subunit 1 of 1, 211 aa, 1 stop
><MW: 24172, pI: 5.99, NX(S/T): 1
MRLFLWNAVLTLFVTSLLIGALIPPEVKIEVLQKPFICHRKTKGGDLMLVHYEGYLEKDGSLL
FHSTHKHNNGQPIWFTLGLILEALKGWDQGLKGMCVGEKRKLIIPPALGYGKEGKGKIPPEST
LIFNIDLLEIRNGPERSHESFQEMDLNDDWKLKDEVKAYLKKEFEKHGAVVNESHHDALVED
IFDKEDEDKDGFISAREFTYKHDEL

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 176-179

Casein kinase II phosphorylation site.

amino acids 143-146, 156-159, 178-181 and 200-203

Endoplasmic reticulum targeting sequence.

amino acids 208-211

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 78-114 and 118-131

EF-hand calcium-binding domain.

amino acids 191-203, 184-203 and 140-159

S-100/ICaBP type calcium binding domain

amino acids 183-203

FIGURE 54

AATAAAGCTTCCTTAATGTTGTATATGTCCTTTGAAGTACATCCGTGCATTTTTTTTTTAGCAT
 CCAACCATTCCTCCCTTGTAGTTCTCGCCCCCTCAAATCACCCCTTCGCCGTAGCCCAACCGA
 CTAACATCTCAGTCTCTGAAATATGCACAGAGATGCCCTGGCTACCTCGCCCTGCCTTCAGCCT
 CACGGGGCTCAGTCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTACACAGTAC
 CTGCCACCCTCAACGTCTCAATGGCTCTGACGCCCGCCCTGCCCTGCACCTTCAACTCCTGTC
 TACACAGTGAACCACAAACAGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTC
 TGAGGAGATGTTCTCAGTTCGCCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAG
 ACCCGTGGAGTTCTCAGGGAACCCAGCAAGTACGATGTGTCCGTGATGCTGAGAAACCTG
 CAGCCGGAGGATGAGGGGATTTACAACCTGCTACATCATGAACCCCCCTGACCGCCACCGTGG
 CCATGGCAAGATCCATCTGCAGGTCTCATGGAAGAGCCCCCTGAGCGGGACTCCACGGTGG
 CCGTGATTGTGGGTGCCCTCCGTCCGGGGCTTCTGGCTGTGGTCACTCTGGTGCTGATGGTG
 GTCAAGTGTGTGAGGAGAAAAAAGAGCAGAAGCTGAGCAGATGACCTGAAGACCGAGGA
 GGAGGGCAAGACCGGCTGAAGGCAACCCGGATGATGGCGCCAAGTAGTGGGTGGCCGGCC
 CTGCAGCCTCCCGTGTCCCGTCTCCTCCCTCTCCGCCCTGTACAGTGACCTGCGCTGCTCG
 CTCTTGGTGTGCTTCCCGTGACCTAGGACCCAGGGCCACCTGGGGCTCTCTGAACCCCG
 ACTTCGTATCTCCACCTGCAACCAAGAGTGACCCACTCTCTTCCATCCGAGAAACCTGCCA
 TGCTCTGGGACGTGTGGGCCCTGGGAGAGGAGAGAAAGGCTCCCACCTGCCAGTCCCTGG
 GGGGAGGCAGGAGGCACATGTGAGGTCCTCCAGAGAGAAAGGAGTGGGTGGGCAGGGGTAGA
 GGAGGGGCCGTGTCACTGCCCCAGTGTCTTGCTGGCAGTGGCTTCAGAGAGGACCTGGTGG
 GGAGGGAGGGCTTCTGTGTGACAGCGCTCCCTCAGGAGGGCTTGGCTGGCACGGCTG
 TGCTCTCCCTGCTCCAGCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCTCTGA
 AACTTGGAGGGGCATGTTAAAGGGATGACTGTGCATTCAGGGCACTGACGGAAGGCCAGGG
 CTGCAGGCAAGCTGGACATGTGCCCTGGCCAGGAGGCCATGTTGGGCCCTCGTTTCCATT
 GCTAGTGGCTCTCTTGGGGCTCCTGTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAG
 ACTGGAAGAGCAGCTCCAGGTAGGGGGCCATGTTTCCAGCGGGGACCCACCAACAGAGGCC
 AGTTTCAAAGTCAGCTGAGGGGCTGAGGGGTGGGGCTCCATGGTGAATGCAGGTTGCTGCA
 GCTCTGCCCTTCTCATGGGGTAACCACTCGCTGGGCAGGGCAGCCAAAGGCTGGGAAAT
 GAGGAGGCCATGCACAGGTGGGGCAGCTTCTTGGGGCTTCAGTGAGAACTCTCCAGTT
 GCCCTTGGTGGGTTTCCACTGGCTTTTGGCTACAGAGAGGGGAAGGGAAGCCTGAGGCCG
 GCATAAGGGGAGGCCTTGGAACTGAGCTGCCAATGCGAGCCCTGTCCCATCTCGCGCCACG
 CTACTCGCTCCTCTCCCAACAACCTCCCTTCTGGGGACAAAGTGACAATTGAGGCCAGGC
 ACAGTGGCTCACGCTGTAACTCCAGCACTTTGGGAGGCCAAGCGGGTGATTACCTCCAT
 CTGTTTAGTAGAAATGGGCAAAACCCATCTCTACTAAAAATACAAGAATTAGCTGGGCGTG
 GTGGCGTGTCCCTGTAATCCAGCTATTGGGAGGCTGAGGCAGGAGAATCGCTTGAGCCCG
 GGAAGCAGAGGTTGCAGTGAACCTGAGATAGTGATAGTGCACATGCAATTACGCTGGGTGAC
 ATAGAGAGACTCCATCTCAAAAAA

10978564-1016160

FIGURE 55

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415
<subunit 1 of 1, 215 aa, 1 stop
<MW: 24326, pI: 6.32, NX(S/T): 4
MHRDAWLPRPAFSLTGLSLFFSLVFPGRSMEVTVPATLNLVNLNGSDARLPCTFNSCYTVNHKQ
FSLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMRLNVQPEDEGI
YNCYIMNPPDRHRGHGKIHLQVLMEEPPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRRK
KEQKLSTDDLKTEEEGKTDGEGNPDDGAK

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 161-179

Immunoglobulin-like fold:

amino acids 83-127

N-glycosylation sites.

amino acids 42-45, 66-69 and 74-77

09973664.101601

FIGURE 56

GTGTATATGTCCTGAAGTACATCCGTGCATTTTTTTTAGCATCCAACCATCCTCCCTTGTA
GTTCTCGCCCCCTCAAATCACCTTCTCCCTTAGCCCACCNACTAACATCTCAGTCTCTGAA
AATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCACGGGGCTCAGTCTCTTTT
TCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCCACAGTACCTGNCCACCCTCAACGTCC
TCAATGGCTCTGACGCCCCGCTGCCCTGCCCTTCAACTCCTGCTACACAGTGAACCACAAAC
AGTTCTCCCTGAACCTGGACTTACCAGGAGTGCAACAACCTGCTCTGAGGAGATGTTCTCCAG
TTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAGACCGCGTGGAGTTCTCAGG
GAACCCAGCAAGTACGATGTGTCGGTGATGCTGAGAAACGTGCAGCCGGAGGATGAGGGGA
TTTACAACTGCTACATCATGAACCCCC

007564.101607

FIGURE 57

TCACGGGGCTCATCTCTTTTCTCTTTGGTGCCACACGAGACGGAGCATGGAGGTNCACATA
CCTGCCACCCCTCAACGTCCTCAATGGCTTTGACGCCCCGCTGCCCTGCACCTTCAACTCCNG
CTACACAGTGAACCACAAACAGTTCTCCCTGAACTGGATTACCAGGAGTGCAACAACCTGGC
TCTGAGGAGATGTTCCCTCCAGTTCCCGCATGGAAGATCATTTAACCTGAAAGCTGGAAGCGG
TTTTCAAGAACCGCGTGGAAGTTCTCAGGGAACCCAGCAAGTACGATGTGTCGGTGATGC
TGAGAAAACGTGCAGCCGGAGGATGAGGGGATTTACAACTGCTACATCATGAACCCCC

0978564-101601

FIGURE 58

TGCGGGGACCGCTGCTACACCATGGGCCCTCCACCTCCGCCCTACCGTGTGGGGCTGCTCCCGGATGGCCTCCTGT
TCTCTTTGCTGCTGCTAAATGCTGCTCGCGGACCCAGCGCTCCCGCGGACGTCAACCCCACTGGTGTCTGGTCC
CTGGTGAATTTGGGTAAACCACTGGAAGCCAAAGCTGGACAAGCCGACAGTGGTGCATCTCTGCTCCAAAGAA
CCGAAAGACTTCTTCAAACTGCGCTGAACTGGAACTGCTGCTGTCTATCTGATGCTGCTGGATTGCAATA
TCAGGCTGGTTTACACAAAACATTCAGGGCCACCCAGTTTCTGTATGGTGTGGATGTACGTGTCTCTGGCTTTG
GGAAGAGCTTTCTCACTGGAGTTTCTGTGAGCCCGAGCAAAAGCAGCGTGGGTTCCTATTTCACACCATGGTGGAGA
GCCTTGTGGCTGGGGCTACACACGGGGTGGAGATGTCCGAGGGGCTCCCTATGACTGGCGCGAGGCCCAAATG
AAAACGGGCCCTACTTCTTGGCCCTCCGCGAGATGATCGAGGAGATGTACAGCTGTATGGGGGGCCCCGTGGTGC
TGGTTGCCACAGATGGGCAACATGTACACGCTCTACTTTTGTGACGGCGAGCCGAGGCTGGAAAGGACAAGT
ATATCCGGGCCCTTGTGTCACTGGGTGCGCCCTGGGGGGCGGTGGCCAAGACCTGCGCGTCTCTGGCTTCAGGAG
ACAAACAACCGGATCCAGTTCATCGGGCCCCCTGAAGATCCGGGAGCAGCAGCGGTGAGCTGTCTCCACAGCTGGC
TGCTGCCCTCAACTACACATGGTCACTGAGAAGTGTTCGTGCAGACACCAACATCAACTACACACTGCGGG
ACTACCGCAAGTCTTCCAGGACATCGGCTTTGAAGATGGCTGGCTCATGCGGCAGGACACAGAAGGGCTGGTGG
AAGCCACGATGCCACCTGGCGTGACGCTGCACTGCGCTTATGGTATGCGCGTCCCCACACAGACTCTCTCTACT
ATGAGAGCTTCCCTGACCGTGACCTAAATCTGCTTTGGTGACGGCGATGGTACTGTGAACCTTGAAGAGTGCCC
TGCACTGCGAGGCTGGCAGAGCGCCGAGGAGCACCAAGTGTGCTGACAGGAGCTGCCAGGCGAGGACATCG
AGATGCTGGCCAACGCCACACCCCTGGCCCTATCTGAACGCTGTGCTCCTTGGGCCCTGACTCTCTGTGCCACAGGA
CTCCTGTGGCTCGGCCGTGGACCTGCTGTTGGCCCTCTGGGGCTGTCTATGGCCCAAGCGTTTTCGAAAGTTTGTGA
CTCACCATTCAAGGCCCGCGAGTCTTGGACTGTGAAGCATCTGCCATGGGGAAGTGTCTTTTGTATCTCTTCTCT
GTGGCAGTGAAGAAGGAAGAAATGAGAGTCTAGACTCAAGGGACACTGGATGGCAAGAAATGCTGCTGATGGTGA
ACTGCTGTGACCTTAGGACTGGCTCCACAGGGTGGACTGGCTGGGCCCTGGTCCAGTCCCTGCTGGGGGCAATG
TGTCCCCCTATTCTGTGGGGCTTTTCACTGTGCTACTGGGCCCTGGGCCCGCAGCTTCTTATGAGGGAGTGT
ACTGGGCTGTGGTCTGTACCCAGAGGTCCAGGGATCGCTCTGCGCCCTCTGGGTGACCTTCCCAACACCA
GCCACAGATAGGCTGCCACTGGTCACTGGTGTAGGTAGCTAGAGCTGCTGGCTTCCCTGTGGCTTAGTGGTGGCCAGCC
TGACTGGCTTCTGGGGGAGCTTAGTAGCTTCTGCGAGGCGGGGAGTTTGTGTGGTCTTCTGTGGTTCACAGGC
CCTGGGACATCTCACTCACTCTTACTCTCTTACCACAGGAGCATTCAGCTCTGGATTGGGCAAGAGATGTG
CCCCAGTCCCGAGGCTGTGTTCCAGGGGCCGTGATTTCCTCGATGTGCTATTGGGCCCGAGGACTGAAGCTGC
CTCCCTTCACTCTGGGACTGTGGTTCAGAGATGAGAGCAGGGGTGGAGCCATGGCTCTTGGAACTTATGGA
GAAAGGGAATCCAAGGAAGCAGCCAGGCTGCTGCGAGCTTCCCTGAGCTGCTGCTTCAACCCACCATCA
CACTGCCACCTTGCCTAGGGTCTCACTAGTAGCAAGTGGGTGAGCACAGGGCTGAGGATGGGGCTCTATCCAC
CTGGGCCAGCACCACCTTAGTGTGGAGTAGCCCGAAACTTGAATGGGACCTGAGAGAGCCAGGGGTCCCC
TGAGCGCCCCCTAGGGCTTTCTGTCTGCCCCAGGGTGTCCATGGATCTCCCTGTGGCAGCAGGCATGGAGAGT
CAGGCTGCCCTTCACTGGCAGTAGGCTTAAGTGGGTGACTGGCCACAGGCGGAGAAAGGGTACAGCCTCTAGGT
GGGTTTCCAAAGACGCCCTTCAGGCTGAGCTGAGCTGCTCTCCACAGGGTTTCTGTGCGAGCTGGATTCTCTGT
TTGTCATACATGCTGGCATCTGTCTCCCTTGTTCCTGAGTGGGCCACATGGGGCTCTGAGCAGGCTGTATCTGT
GATTCTGTCATAAAGTACTCTGGATGCTGTAAAAAAGGAAAAAAAAAAAAA

09978564.101601

FIGURE 59

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44189
><subunit 1 of 1, 412 aa, 1 stop
><MW: 46658, pI: 6.65, NX(S/T): 4
MGLHLRPYRVGLLPDGLLFLLLLLLMLLADPALPAGRHPVVLVPGDLGNQLEAKLDKPTVVH
YLCSKKTESYFTIWLNLLELLLPVIIDCWIDNIRLVYNKTSRATQFPDGVDRVPFGKTFSL
EFLDPSKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPFYFLALREMIEMYQ
LYGGPVLVLAHSMGNMYTLYFLQRQPQAWKDKYIRAFVSLGAPWGGVAKTLRVLASGDNNRI
PVIGPLKIREQQRSVSTSWLLPYNITWSPEKVFVQTPTINYTLRDYRKFFQDIGFEDGWL
MQDTEGLVEATMPPGVLHCLYGTGVPTPDSFYYESFPDRDPKICFGDGDGTVNLKSALQCC
AWQSRQEHQVLLQELPGSEHIEMLANATTLAYLKRVLG

Important features:

Signal peptide:

amino acids 1-28

Potential lipid substrate binding site:

amino acids 147-164

N-glycosylation sites.

amino acids 99-102, 273-276, 289-292 and 398-401

Lipases, serine proteins

amino acids 189-201

Beta-transducin family Trp-Asp repeat

amino acids 353-365

0973551:201601

FIGURE 60

CGGACGCGTGGGCGGACGCGTGGGGCGGCGGCAGCGGCGGCGACGCGGACATGGAGAGCGGG
GCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCTTGACGCAGCCGCA
GGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTCTCTCTGCATCTATGGTG
AGGGCTACAGCAATGCCACGAGTCTAAGCAGATGTACTGCGTGTTC AACCGCAACGAGGAT
GCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCTCTGGCCTCGGCCTTCTTCTTGGT
GGTCGACGCGTATTTCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTG
ACCTGCTCTTCTCAGCTCTCTGGACCTTCTCTGTGGTTTGTGTGGTTTCTGCTTCTCACC AAC
CAGTGGGCAGTCACCAACCGAAGGACGTGCTGGTGGGGGCGGACTCTGTGAGGGCAGCCAT
CACCTTCAGCTTCTTTTCCATCTTCTCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCT
ACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACT
GCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACCTACCAACAGCCACCTTTCACCCAGAA
CGCGGAGACCACCGAGGGCTACGAGCCGCCCCCTGTGTACTTGAGTGGCGGTTAGCGTGGGAA
GGGGGACAGAGAGGGCGCTCCCTCTGCCCCTGGACTTCCCATCAGCCTCCTGGAACTGCCA
GCCCTCTCTTTACCTGTTCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC
TGGCGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCAGAGGGCTTCAGTCAGCCGCT
CACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTTAGCTAGTGTTTTTCTCGCTTTTAATGA
CCTCAGCCCCGCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCT
CAGCTTCCCCCGGCCGGGTGAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAG
ACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGACCAGGCTCTGTGTCTCTCA
CTCAGGTTTGCTTCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCTGTGCCGCT
GGCCTCTGGGCTGCCCTCCCGTGGTGTGAGGGCGGGGCTGGTGTCTATGGCACTTCTCCTTG
CTCCACCCCTGGCAGCAGGAAGGGCTTTGCCTGACAACACCAGCTTTATGTAAATATTC
TGCAGTTGTTACTTAGGAAGCCTGGGAGGGCAGGGGTGCCCATGGCTCCAGACTCTGTCTC
TGTGCCGAGTGATTATAAAATCGTGGGGGAGATGCCCGGCTGGGATGCTGTTTGGAGACG
GAATAAATGTTTTCTCATTTCAAAG

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<subunit 1 of 1, 224 aa, 1 stop

MESGAYGAAGAGGSFDLRRFLTQPVVARAVCLVFALIVFSCIYEGGYSNAHESKQMYCVFN
RNEADACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIIGDLLFSALWTLFLWVFGFC
FLTNTQWAVTNPKDVLVGADSVRAAITFSFSSIFSWGVLASLAYQRYKAGVDDFIQNYVDPTP
DPNTAYASYPGASVDNYQPPFTQNAETTEGYOPPPVY

Type II Transmembrane domain:

Other transmembrane domains:

amino acids 74-90, 108-126 and 145-161

N-glycosylation site.

amino acids 97-100

FIGURE 63

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49152
><subunit 1 of 1, 802 aa, 1 stop
><MW: 88846, pI: 6.41, NX(S/T): 7
MPVAEAPQVAGGQGDGGDEEAEPGMFKACEDSKRKARGYLRLVPLFVLLALLVLASAGVL
LWYFLGYKAEVMVSQVYSGSLRVLNRHFSQDLTRRESSAFRSETAKAQMKELITSTRLGT
YNNSSSVYSFGEGPLTCFFWFILQIPEHRRMLLSPEVVQALLVEELLSTVNSSAAVPYRAEY
EVDPEGLVILEASVKDIAALNSTLGCYRYSYVGQGVLRKGPDLHLASSCLWLHLOGPKDLML
KLRLLEWTLABCDRLAMVDVAGPLEKRLITSVYGCSRQEPVVEVLASGAIMAVVWKGLHSY
YDPFVLSVQPVVFQACEVNLTLNRLDSQGVLSPTYFPSPYSPQTHCSWHLTVPSLDYGLAL
WFDAYALRRQKYDLPTQGQWTIQNRRLCGLRILQPYAERIPVATAGITINFTSQISLTGP
GVRVHYGLYNQSDPCPGEFLLCSVNGLCVPACDGVKDCPNGLDERNCVCRAFQCKEDSTCIS
LPKVCDDGQPDCLNGSDEEQCQEGVFCGTFTFQCEDRSCVKKPNPQCDGRPDGSDGSEEHCD
CGLQGPPSSRIVGGAVSSEGEVNPWQASLQVRGRHICGGALIA DRWVITAAHCFQEDSMASTVL
WTVFLGKVVQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALQLDHPVVRSAAVRPVCLPA
RSHFFEPGLHCWITGWGALREGGPI SNALQKVDVQLIPQDLCSEAYRYQVTPRMLCAGYRKG
KKDACQGDSSGGLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGVISWIIQQVVVT

Important features:

Type II transmembrane domain:

amino acids 46-67

Serine proteases, trypsin family, histidine active site.

amino acids 604-609

N-glycosylation sites.

amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447
and 509-512

Kringle domains.

amino acids 746-758 and 592-609

Homologous region to Kallikrein Light Chain:

amino acids 568-779

Homologous region to Low-density lipoprotein receptor:

amino acids 451-567

0973564.107601

FIGURE 64

GCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGC GCATCCTGCAGCCC
TACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCACTTCACCTCCAGAT
CTCCCTCACCGGGCCCGGTGTGCGGGTGCACTATGGCTTGTACAAACAGTCCGACCCCTGCC
CTGGAGAGTTCCTCTGTCTCTGTAATGGACTCTGTGTCCCTGCCCTGTGATGGGGTCAAGGAC
TGCCCCAACGGCCTGGATGAGAGAAACTGCGTTTGAGAGCCACATTCCAGTGC AAAGAGGA
CAGCATGCATCTCACTGCCCCAAGGTCTGTGATGGGCAGCCTGATTGTCTCAACGGCAGCG
ATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTCACTTCCAGTGTGAGGACCGG
AGCTGCGTGAGAAGCCCAACCCGCAGTGTGATGGGCGGGCCGACTGCAGGGACGGCTCGGA
TGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCTCCAGCCGCATTGTTGGTGGAGCTGTGT
CCTCCGAGGGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTTCGGGGTCGACACATCTGTGGG
GGGGCCCTCATCGCTGACCGCTGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCAT
GGCCTCCACGGTGCTGTGGACCGGTTCCTGGGCAAGGTGTGGCAGAACTCGCGCTGGCCTG
GAGAGGTGTCTTCAAGGTGAGCCGCTGCTCCTGCACCCGTACCACGAAGAGGACAGCCAT
GACTACGACGTGGCGCTGTGTCAGCTCGACCACCGGTGGTGCCTCGGCCCGCTGCGCCC
CGTCTGCCCTGCCCGCGCTCCCACTTCTTCGAGCCCGGCCTGCACTGCTGGATTACGGGCT
GGGGCGCCTTGCGCGAGGGCGGCCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTG
ATCCACAGGACCTGTGCAGCGAGGCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGC
CGGTACCGCAAGGGCAAGAAGGATGCCTGTCAGGGTGACTCAGGTGGTCCGCTGGTGTGCA
AGGCACCTCAGTGGCCGCTGTTCTTGGCGGGGCTGGT CAGCTGGGGCTGGGCTGTGGCCGG
CCTAACTACTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGT
GACCTGAGGAAC TGGCCCCCTGCAAAGCAGGGGCCACCTCCTGGACTCAGAGAGCCAGGGC
AACTGCCAAGCAGGGGGACAAGTAT

FIGURE 65

GGACGAGGGCAGATCTCGTTCTGGGGCAAGCCGTTGACACTCGCTCCCTGCCACCGCCCGG
CTCCGTGCCGCCAAGTTTTCATTTTCCACCTTCTCTGCGCTCCAGTCCCCAGCCCTTGGCCG
AGAGAAGGGTCTTACCGGCCGGGATTGCTGGAAACACCAAGAGGTGGTTTTTGTTTTAA
ACTTCTGTTTTCTTGGGAGGGGGTGTGGCGGGCAGGATGAGCAACTCCGTTCTCTGCTCTG
TTTCTGGAGCCTCTGCTATTGCTTTGCTGCGGGGAGCCCCGTACCTTTTGGTCCAGAGGGAC
GGCTGGAAGATAAGCTCCACAAACCCAAAGCTACACAGACTGAGGTCAAACCATCTGTGAGG
TTTAACCTCCGCACCTCCAAGGACCAGAGCATGAAGGATGCTACCTCTCCGTCCGCCACAG
CCAGCCCTTAGAAGACTGCAGTTTCAACATGACAGCTAAAACCTTTTTTCATCATTACCGGAT
GGACGATGAGCGGTATCTTTGAAACTGGCTGCACAACTCGTGTGAGCCCTGCACACAAGA
GAGAAAGACGCCAATGTAGTTGTGGTTGACTGGCTCCCCCTGGCCACCAGCTTTACACGGA
TGCGGTCAATAATACCAGGGTGGTGGGACACAGCATTGCCAGGATGCTCGACTGGCTGCAGG
AGAAGGACGATTTTTCTCTCGGGAATGTCCACTTGATCGGTACAGCCTCGGAGCGCACGTG
GCCGGGTATGCAGGCAACTTCGTGAAAGGAACGTTGGGCCGAATCACAGGTTTGGATCTCTGC
CGGGCCCATGTTTTGAAGGGGCCGACATCCACAAGAGGCTCTCTCCGGACGATGCAGATTTTG
TGGATGTCCTCCACACCTACACGCGTTTCCTTCGGCTTGAGCATTGGTATTAGATGCCTGTG
GGCCACATTGACATCTACCCCAATGGGGGTGACTTCCAGCCAGGCTGTGGACTCAACGATGT
CTTGGGATCAATTGCATATGGAACAATCACAGAGGTGGTAAAAATGTGAGCATGAGCGAGCCG
TCCACCTCTTTGTTGACTCTCTGGTGAATCAGGACAAGCCGATTTTGCCTTCCAGTGCAT
GACTCCAATCGCTTCAAAAAGGGGATCTGTCTGAGCTGCCGCAAGAACCGTTGTAATAGCAT
TGCTTACAATGCCAAGAAAAATGAGGAACAAGAGGAACAGCAAAATGTACCTAAAAAACCCGGG
CAGGCATGCCTTTTCAGAGGTAAACCTTCAGTCCCTGGAGTGTCCCTGAGGAAGGCCCTTAATA
CCTCCTTCTTAATACCATGTGTCAGAGCAGGGCACATCCTAGCCAGGAGAAGTGGCCAGCA
CAATCCAATCAAATCGTTGCAAATCAGATTACACTGTGCATGTCTTAGGAAAGGGAATCTTT
ACAAAATAAACAGTGTGGACCCCTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAA

0978564.101601

FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49646
><subunit 1 of 1, 354 aa, 1 stop
><MW: 39362, pI: 8.35, NX(S/T): 2
MSNSVPLLCFWSLCYCFAAGSPVPFGPEGRLEDKLHKPKATQTEVKPSVRFNLRSTSKDPEHE
GCYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHLVSAIHRTREKDANVVVDWL
PLAHQLYTDVNNTRVVGHISIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTV
GRITGLDPAGPMPFEGADIHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDF
QPGCGLNDVLGSIAYGTITEVVKCEHERAVHLFVDSL VNQDKPSFAFQCTDSNRFKKGICLS
CRKNRCNSIGYNACKMRNKRNSKMYLKTRAGMPFRGNLQSLCEP

Important features:

Signal peptide:

amino acids 1-16

Lipases, serine active site.

amino acids 163-172

N-glycosylation sites.

amino acids 80-83 and 136-139

FIGURE 67

CGGACGCGTGGGCGGACGCGTGGGCTGGGCAAGGGCCGGGGCGCCGGGCGGAGCCACCTCTTCCCCCTCCCCCGC
TTCCTCTGCGCTCCGCTGGCTGGACGCGCTGGAGGAGTGGAGCAGACACCCGCGGCTGGGGCTGACAGT
CGGCAAAGTTTGGCCCGAAGAGGAGTGGTCTCAAACCCCGGACAGGTGGCGACCGAGCCGACAGGGGCGCTCG
TGCTCTCGGGCGGGCTGTAGGCGAGGGCGCGCCCGAGTGGCGAGACCCGGGCTTACAGAGCTCGGCGGGGAG
AGAAGAGTGGCGGGCGGACGGAGAAACAACTCTCAAAGTTGGCGAAAGGACCGGCCCTACTCCCGGGCTGGCG
CCGCTCCCCCGCCCCAGCCCTGGCATCCAGAGTACGGGTGACGCCCGGGCCATGAGAGCCCCCTGGGGAGGGGG
CACCAGGGAGGCTGGGGCCCCGGGGCTCCGCCCGGACCCCATCGGTAGACCACAGAGCTCCGGGACCCCTTCG
GCACCTCTGGACAGCCCGAGTGTCTGTGGCCACCTCCTCCTCCTCCTCTGGAGGGCGCTCTGGCCCATCCAG
ACCGGATTTATTTTCCAAATCATGCTTGTGAGGACCCCCAGCAGTGTCTTAGAAGTGCAGGGCACCTTTACAGA
GGCCCCCTGTCCGGGACAGCCGACCTCCCTCGCCAACTGCACCTGGCTCATCTCCGGGACGAGGAAACAGAGCT
TCACCATCAGTGTCCAGAGCTACACCTGGCCCTGTGGCTCAGAGCGCTTAACTCCTACGCTCCCTCTCCAGCCAC
TGATCTCCTCTGTGTGAGGACCTCCAGCCCTCTGCAGCTGCCCGGGGGCAACGTACCATCACTTACAGCTATG
CTGGGGCCAGAGACCCATGGGCCAGGGCTTCCTGCTCTCTACAGCCAAAGATTGGCTGATGTGCCCTGCAGGAAG
AGTTTCAGTGCTGAAACACCGCTGTGTATCTGCTGTCCAGCGCTGTGATGGGGTTGATGCTGTGGCGATGGCT
CTGATGAAGCAGGTTGCAGCTCAGACCCCTTCCTGGCCGTGACCCCAAGACCCGTTCCCTCCCTGCTTGAATG
TCACCTTGGAGGACTTCTATGGGGTCTTCTCCTCTCCTGGATATACACACCTAGCCTCAGTCTCCACCCCCAGT
CCTGCCATTGGCTGCTGGACCCCCATGATGGCCGGGGCTGGCGGTGGCTTCAAGCCCTGGACTTGGGCTTTG
GAGATGCAGTGCATGTGTATGACCGCCCTGGGCCCCCTGAGAGCTCCCGACTACTGCTAGTCTCACCCACTTCA
GCAATGGCAAGGCTGTACTGTGGAGACACTGTCTGGCCAGGCTGTGTGTCTACCCACACAGTGTCTTGGAGCA
ATGTTGTGTGCTTCAATGCCACCTACCATGTGCGGGGCTATTGCTTGGCTTGGGACAGACCTGTGGCTTAGGGCT
CTGGCCCTGGGAGCTGGCGAAGGCTAGGTGAGCGCTGTCTACAGTGAGGCACAGCGCTGTGAGCGGCTCATGGGACT
GTGCTGACGGCACAGATGAGGAGGACTGCCAGGCTGCCACCTGGACACTTCCCTGTGGGGCTGTGGCACCT
CTGTTGCCACAGCCTGTACTGTGCTGCTGACCGCTGCAACTACAGACTTCTGTGTGATGGAGCAGATGAGA
GACGCTGTGCGCATTGGCAGCCTGGCAATTTCCGATGCGGGACGAGAAGTGGGTGTATGAGACGTGGGTGTGGCG
ATGGGCGACGAGACTGTGGGACGGCAGTGATGAGTGGACTGCTCTATGCTGCCCCGCAAGCTCATTAACAG
CTGCAGTCAATGGCAGCTAGTGTGCGGCTGCTCCTGGTCACTGCCCTGGGCTGGCACTCCAAGCTCTATGGCA
TTCCGACCCAGAGTACAGCATCTTGGCCCCCTCTCCGGATGGAGGCTGAGATTGTGTCAGCAGCAGGCGACCC
CTCTCTACGGGCGACTCATTGGCCAGGGTGCCATCCCACTCTAGAGACTTTCTTACAGAGAACTCTTAATGATA
ACTCAGTGTGTGGGCACTTGTGCTTCTGCTACAGATCTTACGCGAGATATGCTGTCAGCAGCAGGCGACCC
CCGCGCGTGTGTCAGGGGGCGCTTGTATGCGACGCTGTGACGCGCTCTCCGCGCTGGGCTTGTCTCCCTCGAA
CCACACCCCGCTCTGGGCTCTGAGGCGAGATCCAGGTACACCTTCTGCTGCTCCCTTGGAGCCCTAGATG
GTGGCACAGGCTCAGCCGCTGAGGGCGGGGCGAGTGGGTGGGCAAGATGGGGAGCAGGCACTCCCTGCGCATCA
AGGCTCCCTCCGCTCTGTAGCAGCTCTCAGCCCCACTACTGTCCCTGAAAGCCCCAGGGCCACTGCCCCATC
TGCCCCCTAGAGGCTCACTATCTGTGGAGTGGTGCAGGCCCTGCGAGGGCGGCTTGTGGCCAGCCTGGGGCCCC
CAGGACCAACCCGAGGACTTCTGAGCCCAACAGCAGTCTCTGGCCCTGGAGAGATGAGGACGATGTCTACTGG
TGCCACTGGCTGACCGGGGGTGTGGGTAGCTGAGGCGAGAGGATGAGCACTGCTTACCTTGAAGGGACCTGGGG
CTCTACTGAGGCTCTCCCTGGGCTGCTACTCATAGTGGCACAACCTTTTAGAGGTGGGTGAGGCTCCCTCC
ACCACTTCTCTCCCTGCTGCTGATTTTCAGGACTTGGTGGGCTCCCGTGGACCTATGTAGCTCTGCTATATAAGT
TAAGTGTCCCTCAGGCGAGGAGAGGGCTCACAGAGTCTCCTCTGTACGTGGCCATGGCCAGACACCCAGTCCCT
TCACCAACCACTGCTCCCAAGCCACCACTTTGGGTGGCTGTTTTTAAAGTATAAGTCTTTAGAGGATCATA
GGTCTGGACCTCTCATCTTGGCAAACTCTACCCAAAAGTGGCTTAAAGCACCGGAATGCCAATTAACATAGAGA
CCCTCCAGCCCCCAGGGGAGGATTTGGGCAAGACTTGAAGTTTGGCATCCAATCCCTCTCAAGGGCTCGG
CTCACAAAAGAGTGCAACAAATGCTCTATTCCAAGTACGGCATGTCTCAGTAAGTTGAGGTCAAAAATAAA
GGAATCATACATCTC

09978564.101601

FIGURE 68

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631

<subunit 1 of 1, 713 aa, 1 stop

<MW: 76193, pI: 5.42, NX(S/T): 4

MLLATLLLLLLGGALAHDPRIIFPNHACEDPPAVLLEVGTLQRPLVRDSRTSPANCTWLIL
GSKEQTVTIRFQKLHLACGSERILTLRSPLQPLISLCEAPPSPLQLPGGNVTITYSYAGARAP
MGQGFLLSYSQDWLMCLQEETFQCLNHRCVSAVQRCGDVDACGDGSDAEGCSSDPFPGLTFRP
VPSLPCNVLTEDFYGVFSSPGYTHLASVSHPOQSCHWLLDPHDGRRILAVRFTALDLGFGDAVH
VYDGPGPPESSRLRLSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGNATYHVRGYCLP
WDRPCGLGSGLGAGEGLGERCYSEAQRCDGSDCADGTDDEEDCPGCPPGHFPCGAAGTSGAT
ACYLPADRCNYQTFCADGADERRCRHCQPGNFRCRDEKCVYETWVCDGQPDACDGSDDEWDCS
YVLPRKVITAAVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSY
GQLIAQGAIPVEDFPTENPNDNSVLGNLRSLLQILRQDMTPGGGPGARRRQRGRMLMRLVR
RLRRWGLLPRTNTPARASEARSQVTPSAAPLEALDGGTGPAREGGAVGGQDGEQAPPLPIKA
PLPSASTSPAPTTVPEAPGPLPSLPLEPSLLSGVVQALRGRLLPSLGGPPGPTRSPPGPHTAV
LALEDEDDVLLVPLAEPGVWVAEAEDEPLLT

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 442-462

LDL-receptor class A (LDLRA) domain proteins

amino acids 411-431, 152-171, 331-350 and 374-393

00073564.101601

FIGURE 69

CGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGGTTGCTATCGCTTCG
CAGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCA
GACGCGATGGATAACGTGTCAGCCGAAAAATAAACATCGCCCTTCTGCTTCAGTGTGAAAGG
CCACGTGAAGATGCTGCGGCTGGCACTAACTGTGACATCTATGACCTTTTTTATCATCGCAC
AAGCCCCGTAACCATATATTGTTATCACTGGATTGGAAGTCACCGTTATCTTATTTTTCATA
CTTTTATATGTACTCAGACTTGATCGATTAAATGAAGTGTTATTTTGGCCCTTGCTTGATAT
TATCAACTCACTGGTAACAACAGTATTTCATGCTCATCGTATCTGTGTTGGCACTGATACCAG
AAACCACAACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTCTT
GCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCCAGCGGTCCTTACCAGAAAAA
GCCTGTGCATGAAAAAAGAAGTTTGTAAATTTTATATTACTTTTTTAGTTTGATACTAAGT
ATTAAACATATTTCTGTATTCTTCAAAAAAAAAAAAAAAAAA

0978564-101601

FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49645
><subunit 1 of 1, 152 aa, 1 stop
><MW: 17170, pI: 9.62, NX(S/T): 1
MDNVQPKIKHRPFCFSVKGHVKMLRLALTVTSMTEFFIIAQAPEPYIVITGFVETVILFFILL
YVLRDLRLMKWLFWPLLDIINSLVTTVFMLIVSVLALIPETTTTLTVGGGVFALVTAVCCCLAD
GALIYRKLLFNPSGPYQKKPVHEKKEVL

Important features:

Potential type II transmembrane domain:

amino acids 26-42

Other potential transmembrane domain:

amino acids 44-65, 81-101 and 109-129

Leucine zipper pattern

amino acids 78-99 and 85-106

N-myristoylation site.

amino acids 110-115

Ribonucleotide reductase large subunit protein

amino acids 116-127

0075551-10602
2007-10-23/66

FIGURE 71

GGGCGAGAAGTAGGGGAGGGCGTGTCCGCCGCGGTGGCGGTGCTATCGTTTTGCAGAACC
TACTCAGGCAGCCAGNTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCAGACGCGA
TGGATAACGTGCAGCCGAAAAATAAACATCGCCCCCTTCTGCTTCAGTGTGAAAGGCCACGTG
AAGATGCTGCGGCTGGCACTAACTGNGACATCTATGACCTTTTTTATNATCGCACAAGCCCC
TGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTCATACTTTTAT
ATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTTGGCCTTTGCTTGATATTATCAAC
TCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAGAAACCAC
AACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTINTTGCCGAC

097554.101601

1. Introduction

CAGCCCCGCGCGCCGGCCGAGTCTGCTGAGCCGCGGCTGCGCGGACGGGACGGGACCGGCTAGG
CTGGGCGCGCCCCCGGGCCCCGCGCTGGGCATGGGCGCACTGGCCCCGGGCGCTGCTGCTGC
CTCTGCTGGCCAGTGGCTCTTGCGCGCCGCCCGGAGCTGGCCCCCGCGCCCTTACAGCTGC
CCCCTCGGGTGGCCGCGGCCACGAACCGCTAGTTTGCGCCACCCCGGACCCGGGACCCC
TGCCGAGCGCACGCGCAGCGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCG
GCGCCGCCAACTTCTTGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTA
CTGGAGATGTGTATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAG
TAACTTTGCCGTGGCAGGAACCCCGCACTCTACATAGACAGTACTTTGACACAGAGAGGT
CTAGCACATACCGCTCCAAGGGCTTTGACGTACAGTGAAGTACACACAAGGAAGCTGGACG
GGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAA
CATTGCCACTATTTTTGAATCAGAGAATTTCTTTTGCTGGGATTAAATGGAATGGAATAC
TTGGCTAGCTATGTCCACACATCTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC
CTGGTGACACAAGCAACATCCCCAACGTTTCTTCCATGCAGATGTGTGGAGCCGGCTTGCC
CGTTGCTGGATTCTGGGACCAACGAGGTTGCTTGCTGCTGGTGGAAATTGAACCAAGTTTGT
ATAAAGGAGACATCTGGTATACCCCTATTAAAGGAAGTGTGGTACTACAGATAGAAATTCG
AAATTGGAATTTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGC
CATCGTGGACAGTGGCACCACGCTGTGCGCCTGCCCGAGAAGGTGTTTGATGCGGTGTTGG
AAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTTCTGGACTGGGTCCAG
CTGGCGTGTGAGCAATTCGAAACACCTTGGTCTTACTTCCCTAAATCTCCATCTACCT
GAGAGACGAGAACTCCAGCAGGTCAATTCGTATCACAATCTGCCTCAGCTTTACATTAGC
CCATGATGGGGGCGCGCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCATCCAAAT
GCGCTGGTGATCGGTGCCACGTTGATGGAGGGCTTCTACGTATCTTCGACAGAGCCAGAA
GAGGGTGGGCTTCGACAGCGAGCCCTGTGCAGAAATTGCAGGTGCTCGAGTGTCTGAAATTT
CCGGGCCCTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAG
CCCATTTTGTGGATTGTGTCCATATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCCT
AATCGTCTGTGCTGTGCGGTTCCGGTGTGAGCGTCGCCCCCGTGACCTGAGGTCTGTCA
ATGATGAGTCTCTCTGGTCAGACATCGCTGGAAATGAATAGCCAGGCGCTGACCTCAAGCAA
CCATGAACCTCAGCTATTAAGAAAATCACATTTCCAGGCGAGCAGCCGGATCGATGTTGGCG
CTTTCTCTGTGTCGCCACCGCTCTTCAATCTCTGTTCTGCTCCAGATGCCTTCTAGATTAC
TGTCTTTTGATTCTGATTTTCAAGCTTTCAAATCTCCCTACTTCCAAGAAAAATAATTA
AAAAAAAATCTTATTAA

Dr. J. B. Jones, Jr., 1000 14th St., N.W., Washington, D.C.

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><subunit 1 of 1, 518 aa, 1 stop
```

MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTPGPGTPAERHADGLAL
ALEPALASPAGAAANFLAMVDNLQGDSSRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHS
YIDTYFDTERTSSTYRSKGFDTVVKYTGQSWTGFVGEDLVTIPKGFNTSFLVNIATIPESENF
FLPGIKWNGILGLAYATLAKPSSSLETFPDSLVTQANIPNVFSMQMCGALGPVAGSGTNGGS
LVLGIEPSLYKGDIIWYTPIKEEWYQIEILKLEIGGQSLNLDCREYNADKAIVDSGTTLLR
LPQKVFDVAVVEAVARASLIPEFSDGFWTGSQSLACWTNSETPWSYFPKISIIYLRDENSRSFR
ITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGF AASPCA
EIGAAGVAISEGPFSTEDVASNCVPQAQSLSEPILWIVSYALMSVCGAILLVILVLLLPPRC
ORPRDPEVVNDESSIVRHRWK

Signal peptide:

amino acids 1-20

amino acids 466-494

amino acids 170-173 and 366-369

amino acids 10-31 and 197-118

amino acids 109-118, 252-261 and 298-310

FIGURE 74

CGCCTCCGCCTTCGAGGCTGACGCGCCCGGGCGCGTTCCAGGCCTGTGCAGGGCGGATCG
GCAGCCGCCTGGCGGCGATCCAGGGCGGTGCGGGGCTGGGCGGGAGCCGGAGGCGCGGCC
GGCATGGAGGCGCTGCTGCTGGGCGCGGGGTGCTGCTGGGCGCTTACGTGCTGTCTACTA
CAACCTGTTGAAGGCCCGCCGCTGCGGCGGCATGGGCAACCTGCGGGGCCGACGGCCGTGG
TCACGGGCGCCAAACAGCGGCATCGGAAAGATGACGGCGCTGGAGCTGGCGCGCCGGGGAGCG
CGCGTGGTGCTGGCCTGCCGAGCCAGGAGCGCGGGAGGCGGCTGCCCTTCGACCTCCGCCA
GGAGAGTGGGAACAATGAGGTCATCTTCATGGCCTTGGACTTGGCCAGTCTGGCCTCGGTGC
GGGCCTTTGCCACTGCGCTTTCTGAGCTCTGAGCCACGGTTGGACATCTCATCCACAATGCC
GGTATCAGTTCCTGTGGCCGAGCCCGTGAGGCGTTTAACTGTGCTTCGGGTGAACCATAT
GGTCCCTTTCTGCTGACACATCTGCTGCTGCCTTGCCCTGAAGGCATGTGCCCTAGCCGCG
TGGTGGTGGTAGCCTCAGCTGCCCACTGTGCGGGACGTCTTGACTTCAAACGCGTGGACCGC
CCAGTGGTGGGCTGGCGGCAGGAGCTGCGGGCATATGCTGACACTAAGCTGGCTAATGTACT
GTTTGCCCGGGAGCTCGCCAAACAGCTTGAGGCCACTGGCGTCACCTGCTATGCAGCCCAAC
CAGGGCCTGTGAACCTCGGAGCTGTTCCTGCGCCATGTTCTGGATGGCTGCGCCCACTTTTG
CGCCCATTTGGCTTGGCTGGTGCTCCGGGCACCAAGAGGGGGTCCCAGACACCCCTGTATTG
TGCTCTACAAGAGGGCATCGAGCCCTCAGTGGGAGATATTTTGCCAACTGCCATGTGGAAG
AGGTGCTCCAGCTGCCCGAGACGACCGGGCAGCCCATCGGCTATGGGAGGCCAGCAAGAGG
CTGGCAGGGCTTGGGCTGGGGAGGATGCTGAACCCGATGAAGACCCCACTGTGAGGACTC
AGAGGCCCCATCTTCTAAGCACCCCCACCTGAGGAGCCACAGTTTCTAACCTTACC
CCAGCCCTCAGAGCTCACCAGATTGTCTAAGATGACGCACCGAATTGAGCTAAAGTTGAG
CCTGAGATCCAGCTCTCCTAAACCCTCAGGCCAGGATGCTTGCCATGGCACCTTCATGGTCCTT
GAAAACTCGGATGTGTGTGAGGCCATGCCCTGGACACTGACGGGTTTGTGATCTTGACCTC
CGTGGTTACTTTCTGGGGCCCCAAGCTGTGCCCTGGACATCTCTTTTCTGGTTGAAGGAAT
AATGGGTGATTATTTCTTCTGAGAGTGACAGTAACCCAGATGGAGAGATAGGGGTATGCT
AGACACTGTGCTTCTCGGAAATTGGATGTAGTATTTTCAGGCCCCACCCCTATTGATTCTG
ATCAGCTCTGGAGCAGAGGCAGGGAGTTTGCAATGTGATGCACTGCCAACATTGAGAATTAG
TGAAGTATCCCTTTGCAACCGCTTAGCTAGGTAGTTAAATTACCCCATGTTAATGAAGCG
GAATTAGGCTCCCGAGCTAAGGGACTCGCCTAGGGTCTCAGTGAAGTGGGTGCTGAGAAGTGA
GGATCTGAACCAAGGGTCTGAGGCCAGGGCCGACTGCGGTAAGATGGGTGCTGAGAAGTGA
GTCAGGGCAGGGCAGCTGGTATCGAGGTGCCCCATGGGAGTAAGGGGACGCGCTTCGGGGCGG
ATGCAAGGCTGGGGTCTGCTGATCTGAAGCCCTCGGAATAAAGCGGTTGACCGCCAAAA
AAAAAAAAAAAAAAAA

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FIGURE 75

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48227
<subunit 1 of 1, 377 aa, 1 stop
<MW: 40849, pI: 7.98, NX(S/T): 0
MEALLLGAGLLLGAYVLVYYNLVKAPPCGGMGNLRGRTAVVTGANSIGIGKMTALELARRGAR
VVLACRSQERGEAAAFDLRQESGNNEVIFMALDLASLASVRAFATAFLSSEPRLDILIHNAG
ISSCGRTREAFNLLLRNVNHIGPFLLTHTLLPCLKACAPSRVVVVASAAHCRGRDLDFKRLDRP
VVGWRQELRAYADTKLANVLFARELANQLEATGVTCYAAHPGPVNSELFRLRVPGWLRPLLLR
PLAWLVLRAPRGGAQTPLYCALQEGIEPLSGRYFANCHVEEVPPAARDRAAHLWEASKRL
AGLGPGEDAEPDED PQSEDEAPSSSLSTPHPEPTVSPQYPSPQSSPDLSKMTHRIQAKVEP
EIQLS

Important features:

Signal peptide:

amino acids 1-16

Glycosaminoglycan attachment site.

amino acids 46-49

Short-chain alcohol dehydrogenase family

amino acids 37-49 and 114-124

00078564.10160

FIGURE 77

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41404

<subunit 1 of 1, 985 aa, 1 stop

<MW: 105336, pI: 6.55, NX(S/T): 7

MGMAQDSPPQILVHPQDQLFQGGPARMSCQASGQPPPTIRWLLNQPLSMVPPDPHLLLP
DGTLLLLQPPARGHAHDQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDM
VAVVGEQFTLECGPPWGHPTEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEEKSDEGYMCV
ATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLNPNPDAEGPKPRPAVWLSWKV
SGPAAPAQSYTALFRTQTAPGGQGAPWAEELLAGWQSAELGGLHWGQDYEFKVRPSSGRARG
PDSNVLLLRLEPKVPSAPPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYQVWSLGNSTSLPP
ANWTVVGEQTQLEIATHMPGSYCVQVAAVTGAGAGEPSRPVCLLLEQAMERATQEPSEHGPW
TLEQLRATLKRPEVIATCGVALWLLLLGTAVCIHRRRRARVHLGPGLYRYTSEDAILKHRMD
HSDSQWLADTWRSTSGSRDLSSSSSLSSRLGADARDPLDCRRSLLSWDSRSPGVPLLPDST
FYGLSLIAELPSSTPARSPQVPVAVRRLPPQLAQLSSPCSSSDSLCSRRGLSSPRLSLAPAEA
WKAKKKQELQHANSSPLLRGSHSLELRACELGNRGSKNLSQSPGAVPQALVAVRALGPKLLS
SSNELVTRHLPAPLFPFHETPPTQSQQTQPPVAPQAPSSILLPAAPIPILSPCSPSPQASS
LSGSPPASSRLSSSSSLSLGEDQDSVLTPEEVALCLELSEGEETPRNSVSPMPRAPSPPTTY
GYISVPTASEFTDMGRTGGGVGPKGVLLCPPRPCLTPTPSEGLANGWSASEDNAASARA
SLVSSSDGSLADAHFARALAVAVDSFGFGLPREADCVFIDASSPPSPRDEIFLTPNLSLP
LWEWRPDWLEDMEVSHQTRLGRGMFPWPDPDSQISSQRSQLHCRMPKAGASPDVYS

Important features:

Transmembrane domain:

amino acids 448-467

N-glycosylation sites:

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

N-myristoylation sites.

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

Phosphotyrosine interaction domain proteins

amino acids 740-753

FIGURE 78

CTCCCCAGGTGTCCAGCGCCCAAGATGCGGCTTCTGGTCTGCTATGGGGTTGCCTGCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAGGGGCACTGTGT
 CCTGTCAGTGCACCTACAGGGGAAGAGCTGAGGGACCACCGGAAGTACTGTGCAGGAAGGST
 GGGATCCTCTTCTCTCGTGTCTTGGCACCATCTATGCAGAAAGAAAGGCCAGAGACAAT
 GAAGGGCAGGTGTCATTCGCTGACAGCGCCAGGAGCTCTCGCTCATTTGTACCCCTGTGGA
 ACCTCACCCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCGATGAG
 TCTTTATCTGATCTCTCTGTTCTGCTTTTCCAGGACCCTGCTGTCTCTCCCTTCTCCAC
 CTTCCAGCCTCTGGCTACAACAGCCTGCAGCCCAAGGCCAAAAGCTCAGCAAAACCAGCCCC
 CAGGATTGACTTCTCTGGGCTCTACCCGGCAGCCACCAAGCAAGAGGGGAAAGACAGGG
 GCTGAGGCCCCCTCCATTGCCAGGGACTTCCACAGTACGGGCACGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCCTCACCAGCGACCTCTCCTCTCGAGGGAGCTCCCGCCCCCATGACAGC
 TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG
 GTGTCCATCCCGATGGTCCGCATCTGGCCCCAGTCTGTGTGCTGCTGAGCCTTCTGTGAGC
 CGCAGGCTGTATCGCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAGCTCAACAGGCCA
 CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTACGCTTGACTGCGGAGGAAAAGGAAGCC
 CTTTCCAGGCCCCGTAGGGGGACGTGATCTCGATGCCTCCCCCTCCACATCTGAGGAGGA
 GCTGGGCTTCTCGAAGTTTGTCTCAGCGTACGGGCAGGAGGCCCTCTGGCCAGGCCAGCAGT
 GAAGCAGTATGGCTGGCTGGATCAGCAGCGATTCCCGAAAAGCTTTCACCTCAGCCTCAGAG
 TCCAGTCTGCCGGACTCCAGGGCTCTCCCCACCCTCCCCAGGCTCTCCTCTGTGATGTTTCCA
 GCCTGACCTAGAAGCGTTTGTGACGCCCTGGAGCCAGAGCGGTGGCCTTGTCTTCTCCGGCTG
 GAGACTGGGACATCCCTGATAGGTTTACATCCCTGGGCAGAGTACCAGGCTCTGACCCCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGC
 CTCATGCCAGGTGCGGACCCCTGCGCTTCTCCACTCCAGAGCCCACCTTGTCTTCTCCCTCC
 TGGCGTCTCAGACTAGTCTAGTCCCAAGTCTCCTGCATCAGCTGGGTGATGAAGAGGAGCATGCT
 GGGGTGAGACTGGGATTCTGGGCTTCTCTTTGAACCACTGCATCCAGCCCTCAGGAAGCCCT
 GTGAAAAACGTGATTCTCTGGCCCCCAAGAGACCACAAAACCATCTCTGGGCTTGGTGCAG
 GACTCTGAATTCTAACCAATGCCAGTGAAGTCTGACCTTGAAGTTTGAAGGCCAGTGGGCTG
 ATGAACGCTCACACCCCTTACGCTTAGAGTCTGCATTGGGCTGTGAGCTCTCCACCTGCC
 CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCTCTGAGGCTGTCTAAG
 TCCAGGCTTGGTCAAGTCAAGTGCACATTGCAGGATAAGCCAGGACCGGCCACAGAAGTGG
 TTGCGCTTTCATTTGCGCCTCCCTGGNCCATGCTCTTGTGCTTTGAAAAAATGATGAAGA
 AAACCTTGGCTCCTTCTGTCTGGAAGGGTTACTTGCCTATGGGTTCTGGTGGCTAGAGA
 GAAAAGTAGAAAACAGAGTGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG
 ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTTCGGGGGTGGTGGTAAAGTA
 GCACAAGTCACTATTTTCTTTTCTTTTCCATTATTTATGTTTAAAGACAGAATCTCGTGCT
 GCTGCGCAGGTGGAGTGCAGTGGCAGCATCTGCAAACTCCGCTCCTCGGTTCAAGTGATT
 CTTCTGCCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCCACCACTGGCTAATT
 TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTGGCCAGGCTGGTCTTGAACCTCTGAC
 CTCAAATGAGGCTCTCTGCTTCACTCTCCCAAAATGCGGGGATTACAGGCATGAGCCACTGTG
 TCTGGCCCTATTTCTTTTAAAGTGAATTAAGAGTTGTTCAAGTATCAAACTTGAAGAAAG
 ATGGAGAGAAAAAGAAAGGAAGAAAAAATGTACCCATATGATCTCACCAGAGACTATCAT
 TATTTGCTTTTGTGTACTTCTTCCACTCTTTTCTTCTTCACTAATTTGCGGGTGTGTTCTT
 TTTACAGAGCAATTAATCTTGTATATACAACCTTTGTATCCTGCCCTTTCCACCTTATCGTTCC
 ATCACTTTATTCAGCACTTCTCTGTGTTTACAGACCTTTTATAAATAAAATGTTTCATCA
 GCTGCATAAAAAAAAAAAAAA

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FIGURE 79

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196
<subunit 1 of 1, 332 aa, 1 stop
<MW: 36143, pI: 5.89, NX(S/T): 1
MRLLVLLWGCLLLPGYEALGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGLFSRCS
GTIYAE EEGQETMKGRVSI RDSRQELSLIVTLWNLTLDAGEYWC GVEKRGPD E SLLISLFV
FPGPCCPPSPSPPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGA EAPPLPG
TSQYGHERTS QYTGTS PHPATSP PAGSSRPPMQLDSTSAEDTSPALSSGSSSKPRVSIPMVRI
LAPVLVLLSLLSAAGLIAFC SHLLLWRKEAQQATETQRNEKFWLSRLTAEKEAPSAPEGD
VISMPLHTSEELGFSKFVSA

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128

1007555-438760

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TTGTGACTAAAAGCTGCGCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGA
GCCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCACTGGTCTC
GCTCTGTTGCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCT
GGACTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAA
GCCCTGTTTCTTCTCCTTCTGTGAGTGGACACCGAGGCTGGTGAGCTGCCTGTGATCCCAA
AGCTCAGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCCGCGGCATAGAAGCCAGAG
CAGGGCTCTCAGAAGGCGGTGGTGCCAGCTGGGATCATGTGTTGGCCCTGGTCTGTCTGC
TCAGCTGCCTGCTACCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTG
CTACATGACTTCGGGCTGGACGGATACCGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGC
TTATTTCAACAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACA
ACGGGATCTTCCAGATCAACAGCCGGAGGTGGTGACGAACTCACCCCGAACGTCCCCAAC
GTGTGCCGGATGTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGC
CATGAAGATAACCCAGAGCCTCAGGCTCTGGGTTACTGGGAGGCCTGGAGGCATCACTGCC
AGGGA AAAAGACCTCAATGAATGGGTGGATGGCTGTGACTTCTTAGATGGACGGAACCATGCA
CAGCAGGTGGGAACCTGTGGTTTGGTTCCTGACCTAGGCTTGGGAAGACAAGCCAGCGAATA
AAGCATGGTTGAACGTGAAA

FIGURE 81

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52187

<subunit 1 of 1, 146 aa, 1 stop

<MW: 16430, pI: 5.05, NX(S/T): 1

MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALD
YEADGSTNNGIFQINSRRWCNLTNPVNPVCRMYCSDLLNPNLKDTVICAMKITQEPQGLGY
WEAWRHHCQKDLTEWVDGCDP

Important features:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 67-72

Homologous region to Alpha-lactalbumin / lysozyme C proteins.

amino acids 34-58 (catalytic domain), 111-132 and 66-107

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FIGURE 82

AGCCGCTGCCCCGGGCGGGGCGCCCCGCGGCGGCACCATGAGTCCCCGCTCGTGCTGCGTTT
 GCTGCGCCTCCTCGTCTTCGCGCTTTCTCAGCCGCGCGAGCAAACTGGCTGTACTGGCCA
 AGCTGTGTCGTCGGTGGGGAGCATCTCAGAGGAGGAGACGTGCGAGAAACTCAAGGSCCTGATC
 CAGAGGCAGGTGCAGATGTGAAGCGGAACCTGGAAGTCATGGACTCGGTGCGCCGCGGTGC
 CCAGCTGGCCATTGAGGAGTGCCAGTACCAGTTCCGGAACCGGCGCTGGAACTGCTCCACAC
 TCGACTCCTTGCCCGTCTTCGGCAAGGTGGTGAACGAAGGACTCGGGAGGCGGCCTTCGTG
 TACGCCATCTCTTCGGCAGGTGTGGCCTTTGCAGTGACGCGGCGGTGCAGCAGTGGGGAGCT
 GGAGAAGTGCAGCTGTGACAGGACAGTGCATGGGGTCAGCCCACAGGECTTCAGTGGTCAG
 GATGCTCTGACAACATCGCCTACGGTGTGGCCTTCTCACAGTCGTTTGTGGATGTGCGGGAG
 AGAAGCAAGGGGGCTCGTCCAGCAGAGCCCTCATGAACCTCCACAACATGAGGCCGCGACG
 GAAGGCCATCCTGACACACATGCGGGTGAATGCAAGTGCCACGGGGTGTGAGGCTCCTGTG
 AGGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCCGCCAGGTGGTCAAGCACTGAAGGAG
 AAGTTTGTATGGTGCCACTGAGGTGGAGCCACGCCGCGTGGGCTCCTCCAGGSCACTGGTACC
 ACGCAACGCACAGTTCAGGCCGACACACAGATGAGGACCTGGTGTAACCTGGAGCCTAGCCCCG
 ACTTCTGTGAGCAGGACATGCGCAGCGGCGTGTGGGCACGAGGGGCGGCACATGCAACAAG
 ACGTCCAAGGCCATCGACGGCTGTGAGCTGCTGTGCTGTGGCCGCGGCTTCCACACGCGCGCA
 GGTGGAGCTGGTGAACGCTGCAGCTGCAAAATCCACTGGTGTGCTTCGTCAAGTGCCGGC
 AGTGCCACGGGCTCGTGGAGTTGCACAGCTGCCGATGACCGCCTGCCTAGCCCTGCGCCGGC
 AACCACCTAGTGGCCAGGGAAGGCCGATAATTTAAACAGTCTCCACCACCTACCCCAAGA
 GATACCTGGTTGTATTTTTTGTCTCTGTTTGGTTTTTGGGTCTCATGTTATTTATTGCCGAA
 ACCAGGCAGGCAACCCCAAGGGCACCAACCAGGGCCTCCCCAAAGCCTGGGCCTTTGTGGCT
 GCCACTGACCAAGGGACCTTGCTCTGTGCCGCTGGCTGCCCGCATGTGGCTGCCACTGACCA
 CTCAGTTGTTATCTGTGTCCGTTTTTCTACTTGACAGACCTAAGGTGGAGTAACAAGGAGTAT
 TACCACCACATGGCTACTGACCGTGTCTATCGGGGAAGAGGGGGCCTTATGGCAGGGAATA
 GGTACCGACTTGATGGAAGTCACACCCTCTGGAAAAAAGAACTCTTAACTCTCCAGCACACA
 TACACATGGACTCCTGGCAGCTTGAGCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGG
 GAACAAGCAGATAACAGGTCAAGGGCACCAAGGTTTCATTTAGCCCTTACATGGACAGCTAGA
 GGTTCGATATCTGTGGGTCTTCCAGGCAAGAAGAGGAGATGAGAGCAAGAGACGACTGAA
 GTCCACCCCTAGAACCCAGCCTGCCCCAGCCTGCCCTGGGAAGAGGAAACTTAACCACTCC
 CCAGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACCAGGGATCCCGGCTGTGCCTT
 TGCAGTCATGCCGAGTCACCTTTACAGCGCTGTTCCTCCATGAAACTGAAAAACACACAC
 ACACACACACACACACACACACACACACACACACAGGACACACACACACACCTGCGAGA
 GAGAGGGAGGAAGGGCTGTGCCCTTTCAGTCATGCCCAGTCACCTTTCACAGCACTGTTCTCT

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FIGURE 83

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328
<subunit 1 of 1, 351 aa, 1 stop
<MW: 39052, pI: 8.97, NX(S/T): 2
MSPRSCRLRSLRLLVFAVFSAAASNWLYLAKLSSVGSISEEETCEKLKGLIQRQVQMCKRNLE
VMDSVRRGAQLAIEECQYQFRNRNRWNCSTLDSLFPVFGKVVTQGTREAAFVYAISSAGVAFV
TRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYGVAFSQS FVDVRERSKGASSSRALM
NLHNEAGRKA I LTHMRVECKCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRR
VGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTSKAIDGCELLC
CGRGFHTAQVELAERCSCKPHWCCFVKCRQCQRLVELHTCR

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 88-91 and 297-300

Wnt-1 family signature.

amino acids 206-215

Homologous region to Wnt-1 family proteins

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

19970504-101601

FIGURE 84

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCAT
CGCCATGGACACCAACAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCGGAGGGC
CCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCTCTTCTTGGCCCTGGCTGTCTCTGGTC
ACCACAGTCTCTTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGC
GGCGCTGCTTGACGGCCACGACCTGCTGAGGACAAACGCTCGAAGCAGACGGCGCGCTGG
GTGCCCTGAAGGAGGAGGTGCGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTG
CAGACCACGCGCGCGGAGCTTGGGGAGGCGCAGGCCAAGCTGATGGAGCAGGAGAGCGCCCT
GCGGGAAGTGCCTGAGCGCGTGACCCAGGCTTGGCTGAAGCCGCGAGGGGCCGTGAGSACG
TCCGCACTGAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACCTCCTGCGAGCCG
TGCCCCACGTCGTGGCTGTCTTTCGAGGGCTCCTGCTACTTTTTTCTCTGTGCCAAAGACGAC
GTGGGCGGCGGCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCC
TGGATGAGCAGGGCTTCTCACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCTGAGG
GCTGTGCGCCATCTGGGCAAGGTTTCAGGGCTACCAGTGGGTGGACGGAGTCTCTCTCAGCTT
CAGCCACTGGAACGAGGAGAGCCCAATGACGCTTGGGGCGCGAGAACTGTGTCTATGATGC
TGACACGCGGGCTGTGGAACGACGACCGGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAG
AAAAGGCACAAGTGTGACCCCGCCAGTGCCCTGGAGCCGCGCCCCATTGCAGCATGTCTGA
TCCTGGGGGCTGCTCACCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTTCTCTCT
CATCCACCGCTGCTGAGTCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCGAGTGCC
TGGGCTCTGGGACCTCCATGCCGACCTCATCTAACTCCACTCACGCAGACCCAACTAACC
TCCACTAGCTCCAAAATCCCTGCTCCTGCGTCCCCGTGATATGCCTCCACTTCTCTCCCTAA
CCAAGGTTAGGTGACTGAGGACTGGAGCTGTTTGGTTTTCTCGCATTTTCCACCAAAGTGA
AGCTGTTTTTGCAGCCTGAGGAAGCATCAATAAATATTGAGAAATGAAAAA

097854-10601

FIGURE 85

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352
<subunit 1 of 1, 293 aa, 1 stop
<MW: 32562, pI: 6.53, NX(S/T): 2
MDTTRYSKWGGSEEVPGGPWGRVWHWSRRPLFLALAVLVTTLWAVILSILLSKASTERAA
LLDGHDLLRTNASKQTAALGALKEEVDCHSCCSGTQAQLQTTRAE LGEAQAKLMEQESALR
ELRERV TQGLAEAGRGREDVRTELFRAL EAVRLQNN SCEPCPTSWLSFEGSCYFFSVPKTTW
AAQDHCADASAHLVIVGG LDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFS
HWNQGE PNDAWGREN CVMMLHTGLWNDAPCDSEKDGWICEKRHNC

Important features:

Type II transmembrane domain:

amino acids 31-54

N-glycosylation sites.

amino acids 73-76 and 159-162

Leucine zipper pattern.

amino acids 102-123

N-myristoylation sites.

amino acids 18-23, 133-138 and 242-247

C-type lectin domain signature.

amino acids 264-287

FIGURE 86

GCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTCGTGGGCAGGGCGAGTTGGGAAAGCG
GCAGCCCCCGCGCCCCCGCAGCCCTTCTCCTCCTTTCTCCACGTCCTATCTGCCTCTCG
CTGGAGGCCAGGCCGTGCAGCATCGAAGACAGGAGGAACTGGAGCCTCATTGGCCGCGCCGG
GGCGCCGGCTCGGGCTTAAATAGGAGCTCCGGGCTCTGGCTGGGACCCGACCGCTGCCGGC
CGCGCTCCCGTGCTCCTGCGCGGTGATGGAACCCAGCCCGCGCCCGCTTGGGCAAG
GCCCTCTGCCTCTCCTCCTGGCCACTCTCGGCGCCGCGGCCAGCCTCTTGGGGGAGAGTC
CATCTGTTCCGCGAGAGCCCCGGCCAAATACAGCATCACCTTCACGGGCAAGTGGAGCCAGA
CGGCCTTCCCAAGCAGTACCCCCCTGTTCCGCCCCCTGCGCAGTGGTCTTCGCTGCTGGGG
GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACCAGTACGTAGTAACGGGCTGCG
CGACTTTGCGGAGCGCGCGAGGCCCTGGGCGCTGATGAAGGAGATCGAGGCGCGGGGGAGG
CGCTGCAGAGCGTGACAGAGGTGTTTTTCGGCGCCCGCGCTCCCCAGCGGCACCGGGCAGACG
TCGGCGGAGCTGGAGGTGCAGCGCAGGCACTCGCTGGTCTCGTTTGTGGTGCGCATCGTGCC
CAGCCCCGACTGGTTCTGTGGCGGTGGACAGCCTGGACCTGTGCGACGGGGACCGTTGGCGGG
AACAGGCGGCGCTGGACCTGTACCCCTACGACGCGCGGACGACAGCGGCTTCACCTTCTCC
TCCCCAACTTCGCCACCATCCCGCAGGACACGGTGACCGAGATAACGTCTCTCTCCAG
CCACCGGCCAACTCCTTCTACTACCCGCGGCTGAAGGCCCTGCCTCCCATCGCCAGGCTGA
CACTGCTGCGGCTGCGACAGAGCCCCAGGGCCTTCATCCTCCCGCCCGAGTCTGCCCCAGC
AGGGACAATGAGATTGTAGACAGCGCCTCAGTTCAGAAACGCCGCTGGACTGCGAGGTCTC
CCTGTGGTCTGCTCTGGGGAAGTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGA
CTCGCTACGTCCGGGTCAGCCCGCAACAACGGGAGCCCTGCCCGAGCTCGAAGAAGAG
GCTGAGTGCGTCCCTGATAACTGCGTCTAAGACCAGAGCCCCGAGCCCCCTGGGGCCCCCG
GAGCCATGGGGTGTCGGGGGCTCCTGTGCAGGCTCATGTGACAGGCGGCCGAGGGCACAGGG
GGTTTCGCGCTGCTCCTGACCGCGGTGAGGCCGCGCGGACCATCTCTGCACTGAAGGCCCT
CTGGTGGCCGGCAGGGCATTGGGAAACAGCCTCCTCCTTTCCCAACCTTGCTTCTTAGGGG
CCCCCGTGTCCTGTCTCTCAGCCTCCTCCTCTGACAGGATAAAGTCATCCCAAGGCTC
CAGCTACTCTAAATTATGTCTCCTTATAAGTTATTGTCTGCTCCAGGAGATTGTCTCTCATCG
TCCAGGGGCTGGCTCCACGTTGGTTGCAGATACCTCAGACCTGGTGTCTAGGCTGTGCTG
AGCCCACTCTCCCGAGGGCGCATCCAAGCGGGGCCACTTGAGAAGTGAATAAATGGGGCGG
TTTCGGAAGCGTCAGTGTTCATGTTATGGATCTCTCTGCGTTTGAATAAAGACTATCTCT
GTTGCTCACAAAAA

097854-10101

FIGURE 87

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53971
><subunit 1 of 1, 331 aa, 1 stop
><MW: 35844, pI: 5.45, NX(S/T): 2
MENPSPAAALGKALCALLLATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAPPKQYPL
FRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAEERGEAWALMKEIEAAGEALQSVHEVF
SAPAVPSGTGQTSAELEVQRRHSLVSFVVRIVPSPDWFGVDSLDCDGRWREQAALDLYP
YDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLLRLRQSP
RAFIPPAPVLP SRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGRLGTKSRTRYVRVQPA
NNGSPCPELEEEAECPDNCV

Important features:

Signal peptide:

amino acids 1-26

109771-4958760

FIGURE 88

GGCGGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTGTTGGTGTCCTGTCTTGCGTGAT
TATTGACAAACTGAAGCTTTTCCTGCACCACTGGACTTAAGGAAGAGTGACTCGTAGCGGA
CAGCTTTAGTGGCCGGCCGGCGCTCTCATCCCCGTAAGGAGCAGAGTCCCTTTGTACTGAC
CAAGATGAGCAACATCTACATCCAGGAGCCTCCCACGAATGGGAAGGTTTTATTGAAAACTA
CAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTGCAGAAATTTT
ATCCAACTTTGTTTGGAAAGCTTATTATGACAAATACCATTTTTCATAGAGTTGTGCCTGGTTT
CATAGTCCAAGCGGAGATCCTACTGGCACAGGAGTGGTGGAGAGTCTATCTATGGAGCGC
CATTCAAAGATGAATTTCACTCACGTTGCGTTTTAATCGGAGAGGACTGGTTGCCATGGCA
AATGCTGGTTCTCATGATAATGGCAGCCAGTTTTTCTTACACTGGGTCGAGCAGATGAACT
TAACAATAAGCATACCATCTTTGGAAAGGTTACAGGGGATACAGTATATAACATGTTGCGAC
TGTCAGAAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAAATAAAGCTGT
GAGGTTTTGTTTAACTCCTTTTGATGACATCATTTCAAAGGGAATTAAGGCTGAAAAAGA
GAAACCAAGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAATTTTAGTTTACTTT
CATTGGAGAGGAAGCTGAGGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAG
GGCAAAAGCAAAAGTAGTCATGACTTGCTTAAGGATGATCCACATCTCAGTTCTGTTCAGT
TGTAAGAAAGTAAAAAGGTGATGCACCAGATTTAGTTGATGATGGAGAAGATGAAAGTGCAG
AGCATGATGAATATATTGATGGTGTGATAAGAAACCTGATGAGAGAAAGAATTGCCAAAAAA
TTAAAAAAGGACACAAGTGCGAATGTTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATC
AGTCAGCCGCGAGTGAAGAGCTCAGAAAAGAAGCAAGACAATTAACGGGAAGTCTTAGCAG
CAAAACAAAAAAGTAGAAAATGCAGCAAAACAAGCAGAAAAAAGAGTGAAGAGGAAGAA
GCCCTCCAGATGGTGCTGTTGCCGAATACAGAAGAGAAAAAGCAAAAGTATGAAGCTTTGAG
GAAGCAACAGTCAAAGAAGGGAATTTCCCGGGAAGATCAGACCCTTGCACTGCTGAACCACT
TTAAATCTAAACTCACTCAAGCAATTGCTGAAACACCTGAAAATGACATTCCTGAAACAGAA
GTAGAAGATGATGAAGGATGGATGTACATGTACTTCAGTTTGAGGATAAAGCAGAAAAGT
GAAAGATGCAAGCATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCAGTGA
ATAAAAGAAGGAGGGAAGAAAGCAAAAGCTGATGAGAGAGAAAAAGAAAGAAGATATAAAT
GAGAATAATGATAACAGAACTTGCTGGAATGTGCCTACAATGGCCTTGTAAACAGCCATTG
TTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTTGAACCTGTTGTCTGGTTTTG
AAAAACAATTATCTTGTTTTGCAAAATGTGGAATGATGTAAGCAAAATGCTTTTGGTTACTGG
TACATGTGTTTTTCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAACTTTCTCT
TCCACAAAAA

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FIGURE 89

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919
><subunit 1 of 1, 472 aa, 1 stop
><MW: 53847, pI: 5.75, NX(S/T): 2
MSNIYIQEPPTNGKVLLKTTAGDIDIELWSKEAPKACRNFIQLCLEAYYDNTIFHRVVPGFI
VQGGDPTGTGSGGESIYGAPFKDEFHSLRFPNRRGLVAMANAGSHDNQSQFFFTLGRADELN
NKHTIFGKVTGDTVYNMLRLSEVDIDDDERPHNPHKIKSCEVLFPDDIIPREIKRLKKEK
PEEEVKKLKPKGTKNFSLLSFGEEAESEEEVNRVSQSMKGKSKSSHDLKDDPHLSSVPV
ESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKKLKKDTSANVKSAGEGEVEKKSV
SRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEAPPDGAVA EYRREKQKYEALRK
QQSKKGTSREDQTLALLNQFKSKLTQAIAETPENDIPETEVEDDEGWMShVLQFEDKSRKVK
DASMQDSDTFEIYDPRNPVNKRREESKKLMREKKERR

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 109-112 and 201-204

Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.

amino acids 49-66

Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase

amino acids 96-140, 49-89 and 22-51

FIGURE 90

CGCCGCCGTTGGGGCTGGAAGTTCCCGCCAGGTCCTGTCGGGCGAGAGAGATGCTGCCCGG
 CCCGCTCCGGCTTTGAGGCGAGAGAAGTGTCCACAGACCCATTTCGCCTTGCTGACGGCGTCG
 AGCCCTGGCCAGACATGTCCACAGGGTTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACC
 GTGGCGCGCGGGGACCAGCACAGGCGGCGTTTCTCCTTCGGAAACGGGAACGTCTAGCAA
 CCCTTCTGTGGGGCTCAATTTTGGAAATCTTGGAGTACTTCAACTCCAGCAACTACATCTG
 CTCCTTCAAGTGGTTTGGGAACCGGGCTCTTTGGATCTAAACCTGCCACTGGGTCACTCTA
 GGAGGAACAAATACAGGTGCTTGCACACCAGAGGCCTCAAGTGGTCACCAAAATATGGAAC
 CCTGCAAGGAAAAAGATGATGTGGGGAAGACACCCATCCAAGTCTTTTTTAGGAGTCCCT
 TCTCCAGACCTCCTCTAGGTATCCTCAGGTTTGACCTCCAGAACCCTGGAGCCCTGGGAAA
 GGAATCAGAGATGCTACCACCTACCCGCTGGATGGAGTCTCGCTCTGTGCGCAGGCTGGAG
 TGCAGTGGCAGATCTCGGCTACTGCAACCTCCGCTCCCGGGTTCAAGCGAGTCTCCTGC
 CTCAGCCTCTGAGTGTCTGGGGCTACAGGTGCCCTGCAGGAGTCCCTGGGGCCAGCTGGCCCTG
 ATGTACGTCAGCACGCGGGAACGTTACAAGTGGCTGCGCTTACGCGAGGACTGTCTGTACCT
 GAACGTGTACGCGCGCGCGCGCGCCGGGGATCCCGAGCTGCCAGTGTATGGTCTGGTTCC
 CGGGAGGCGCCTTCATCGTGGCGCTGCTTCTTGTACAGGGCTCTGACTTGGCGCGCCGC
 GAGAAAGTGGTCTGTTGTTTCTGCAGCACAGGCTCGGCATCTTCGGCTTCCTGAGCACGGA
 CGACAGCCACGCGCGCGGGAACCTGGGGCTGCTGGACAGATGGCGGCTCTGCGCTGGGTGC
 AGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCTGTTTCGGCCAGTTCGGCG
 GGGGCCATGAGCATCTCAGGACTGATGATGTACACCTAGCCTCGGCTCTCTTCCATCGGGC
 CATTTCCAGAGTGGCACCCGCTTATTCAGACTTTTTCATCACTAGTAACCCACTGAAAGTGG
 CCAAGAGGTTGCCACCTGGCTGGATGCAACCACAACAGCACAGATCCTGGTAAACTGC
 CTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGATGAGATTCTCCAAC
 GAATTCACAGAGAGACCCGGAAGATTTATCTGTTCCATGAGCCCTGTGGTGGATGGTGTGG
 TGATCCAGATGACCTTTGGTGTCTCTGACCCAGGGGAAGTTTTCATCTGTGCCCTACTT
 CTAGGTGTCAACAACTTGAATTCATTTGGCTCTTGCTTATAATATCACCAGGAGCAGGT
 ACCACTTGTGGTGGAGGAGTACCTGGACAAATGTCAATGAGCATGACTGGAAGATGCTACGAA
 ACCGTATGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCACACTGCAGACTGCTCAC
 TACCACCGAGAAACCCCAATGATGGGAATCTGCCCTGTGGCCACGCTACAACAAGGATGAA
 AAGTACCTGCAGCTGATTTTACCACAAGAGTGGGCATGAGCTCAAGGAGAAGAAGATGGC
 TTTTGGATGAGTCTGTACAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGC
 TATGACGGAAGGAGCCAAAGAGGGGTTTGCCCCCACCATCCAGGCCCTGGGGAGACTAGCCA
 TGGACATACCTGGGGACAAGATTCTACCCACCCAGTTTAGAACTGCAGGAGCTCCCTGCT
 GGCTCCAGGCAAAAGCTAGAGCTTTTGCTGTGTGTGGGACTGCACCTGCCCTTTCCAGCC
 TGACATCCCATGATGCCCCCTACTTCACTGTTGACATCCAGTTAGGCCAGGGCCTGTCAAC
 ACCACAGTGTGCTCAGCTCTCCAGCTCCAGGACAACCTCTTTTTCCTCTTTCAAACTCT
 CCCACCTTCAATGTCTCCTTGTGACTCCTTCTTATGGGAGGTGACCCAGACTGCCACTGC
 CCGTGTACCTGCACCCAGCTTGGCATTTACCATCCTCTGCTCAACCTTGTCTCTGTGT
 TCACATTGGCCTGGAGGCCTAGGGCAGGTTGTGACATGGAGCAAACTTTTGGTAGTTTGGGA
 TCTTCTCTCCACCCACACTTATCTCCCCAGGGCCACTCCAAGTCTATACACAGGGGTGG
 TCTCTTCAATAAAGAAAGTGTGATTAGAAAAA

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<subunit 1 of 1, 545 aa, 1 stop

MSTGTSFSGSGLGSTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTSAPSSG
FGTGLFGSKPATGFTLGGTNTGALHTRKRPQVVTKYGTLQGKQMHVGKTPIQVFLGVPFSSRPP
LGILRFAPPEPEPEFWKGI R DATTYPPGWSGLSPGWSAVARSRLTATSASRVQASLLPQPLS
VWGYRCLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVYAPARAPGDPQLPVMVWVPPGGAF
IVGAASSYEGSDLAAREKVVVLVFLQHRLGIFGLSTDDSHARGNWGLLDQMAALRWVQENIA
AFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVA
HLACGNHNSTQILVYNCLRALSGTKVMVRSNKMRFLQLNFQDPEEIIWSMSPVVDGCVIPDD
PLVLTLQKSVSSPYALHGVNNLEKFNWNLPNKMTKEQVPLVVEEYLDNVNEHDWKLNRNRMD
IVQDATFYATLTOTAHYHRETPMMGI CPAGHATTMRKSTSCSILPOEWA

Signal peptide:

Carboxylesterases type-B serine active site.

amino acids 312-327

Carboxylesterases type-B signature 2.

amino acids 218-228

N-glycosylation sites.

amino acids 318-321, 380-383 and 465-468

FIGURE 92

GAGAACAGGCCTGTCTCAGGCAGGCCCTGCGCCTCCTATGCGGAGATGCTACTGCCACTGCT
 GCTGTCTCGCTGCTGGGGCGGGTCCAGGCTATGGATGGGAGATCTTGGATACAGTGCAGG
 AGTCAGTGTATGGTGCCGGAGGGCTGTGCATCTGTGCCCCTGCTCTTCTCCTACCCCGA
 CRAAGACTGGACAGGGTCTACCCAGCTTATGGCTACTGGTTCAAAGCAGTGACTGAGACAAC
 CAAGGCTGCTCCTGTGGCCACAAACCACAGAGTCGAGAGGTGGAAATGAGCACCACCGGGGCC
 GATTCCAGCTCACTGGGGATCCCGCAAGGGAACTGCTCCTTGGTGATCAGAGACGCGCAG
 ATGCAGGATGAGTCAACGACTCTCTTTCGGGTGGAGAGAGGAAGCTATGTGACATATATTT
 CATGAACGATGGGTTCTTTCTAAAGTAAACAGTGCTCAGCTTACGCCAGACCCAGGACC
 ACAACACCGACCTCACCTGCCATGTGGACTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACC
 GTCCGACTCCGTGTGGCCTATGCCCCAGAGACCTTGTATCAGCATTTCACGTGACAACAC
 GCCAGCCCTGGAGCCCCAGCCCCAGGAAATGTCCCATACCTGGAAGCCCAAAAGGCCAGT
 TCCTGCGGCTCCTCTGTGCTGTGACAGCAGCCCCCTGCCACACTGAGCTGGGTCTGTCAG
 AACAGAGTCTCTCCTGTCCTCATCCCTGGGGCCTAGACCCCTGGGGCTGGAGCTGCCCGG
 GGTGAAGGCTGGGGATTACAGGCGCTACCTGCCCAGCGGAGAACAGGCTTGGCTCCAGC
 AGCGAGCCCTGGAGCTCTCTGTGCAGTATCTCCAGAGAACCTGAGAGTGATGGTTTCCAA
 GCAACACGAGACGTCTCTGGAACACCTTGGGAACGGCAGTCTCTCCAGTACTGGAGGGCCA
 AAGCCTGTGCTGGTCTGTGTACACACAGCAGCCCCCAGCCAGCTGAGCTGGACCCAGA
 GGGGACAGGTTCTGAGCCCTCCAGCCCTCAGACCCCGGGGTCTCGAGCTGCCCTCGGGTT
 CAGTGTGAGCACCAAGGAGAGATTACCTGCCAGCTCGGCACCACTGGGTCTCCAGCAGT
 CTCTCTCAGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGGCATTCTCCAACGGAG
 CGTTTCTGGGAATCGGCATCAGGCTCTCTTTTCTCTGCTGGCCCTGATCATCATGAAG
 ATTCTACCGAAGAGACGGACTCAGACAGAAACCCGAGGCCAGGTTCTCCCGGCACAGCAC
 GATCTCGGATTACATCAATGTGGTCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAGA
 AAGCCACACCAAAACAGTCTCGGACCCCTCTCCACAGAGGTCTCCCTCCCAAGATCAAG
 AAGAACAGAAAAAGCAGTATCAGTTGCCAGTTTCCAGAACCCAAATCATCCATCAAGC
 CCCAGAATCCCAGGAGAGCCAAAGAGGAGCTCCATTATGCCACGCTCACTTCCAGGCGTCA
 GACCCAGGCTGAGGCCCGGATGCCAAGGGCACCCAGGCGGATTATGCAGAGTCAAGTTT
 CAATGAGGGTCTCTTAGGCTTTAGGACTGGGACTTCGGCTAGGGAGGAAGGTAGAGTAAGAG
 GTTGAAGATAACAGAGTGCAAGTTTCTTCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCT
 CTCTCTTCTCTCTCTTTAAAAAAACATCTGGCCAGGGCACAGTGGCTCAGCCCTGTAATC
 CCAGCACTTTGGGAGGTTGAGGTGGGCAGATCGCCTGAGGTGGGAGTTTCAGAGCCAGCCTG
 GCCAACTTTGGTGAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGCATGGTGGCAGG
 CGCCTGTAATCTTACCTACTTTGGGAAGCTGAGGCAGGAGAATCACTTGAACCTGGGAGACGG
 AGGTTGCAGTGAGCCAAAGTACACCACTTGACGCGCAGCCTGGGCAACAAAGCGAGACTCCA
 TCTCAAAAAAAAATCTCCAAATGGGTTGGGTGTCTGTAAATCCAGCACTTTGGGAGGCTA
 AGGTGGGTGGATTGCTTGAGCCAGGAGTTCAGAGCCAGCCTGGGCAACATGGTGAAACCCC
 ATCTCTCAAAAAATACAAACATAGCTGGGCTTGGTGGTGTGTGCTGTAGTCCGACCTGT
 CAGACATTTAAACCAGAGCAACTCCATCTGGAATAGGAGCTGAATAAAATGAGCTGAGACC
 TACTGGGTGCACTTCTCAGACAGTGGAGGCATTCTAAGTCAAGGATGAGACAGGAGGTCCG
 TACAAGATACAGGTATAAAGACTTTGCTGATAAAACAGATTGCACTGAAGAAGCAACCA
 ATCCACCAAAACCAAGTTGGCCACGAGAGTGACCTCTGGTCTGCTCTCACTGCTACACTCT
 GACAGCCCATGACAGTTTACAAATGCCATGGCAACATCAGGAAGTTACCCGATATGTCCCA
 AAAAGGGAGGAATGAATAATCCACCCTTGTGTAGCAATAAGCAAGAAATAACCATAAAA
 GTGGGCAACCAGCAGCTCTAGGCGCTGCTCTGTCTATGGAGTAGCCATTCTTTTGTCTCT
 TACTTTCTTAATAAAGTTGCTTTCACCTTAAAAAA

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FIGURE 93

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002

><subunit 1 of 1, 544 aa, 1 stop

><MW: 60268, pI: 9.53, NX(S/T): 3

MLLPILLSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWFK
AVTETTKGAPVATNHQSREVEEMSTRGRFQLTGDPAGKNCSLVIRDAQMQDESQYFFRVERGS
YVTYNFMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVIS
ISRDNTPALEFPQPQGNVPYLEAQKGQFLRLCAADSQPPATLSWVLQNRVLSSSHPWGPRPL
GLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENLNGTSL
PVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHP
LGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALFLCLALIIMKILPKRRTQTETPRPR
FSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESKKNQKKYQLPSFPEP
KSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ

Important features:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 100-103, 297-300 and 306-309

**Immunoglobulins and major histocompatibility complex proteins
signature.**

amino acids 365-371

1007-1982-550

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TGAAGAGTAATAGTTGGAATCAAAGAGTCAACGCAATGAACATGTTATTTACTGCTGCGGTTT
TATGTTGGGAATTCCTCTCTCTATGGCCCTTGTCTTGGAGCAACGAAACATCTCCAAACAAAGA
AAGTCAAGCAGCAGTGCAGTACTCTATTGAGAGTGAAGCGTGGCTGGGTGTGGGAACCAATTT
TTTGTACACAGAGGAAATGAATACGACTAGTCATCACATCGGCCAGCTAAGATCTGATTTAGA
CAATGGAAACAATCTTTCCAGTACAAGCTTTTGGGAGCTGGGAGCTGGAAGTACATTTTATCA
TTGATGAAAGAAACAGTGCAGATATAGCATACAGAAAGCTTGATAGAGAGGAGCGATCCCTC
TACATCTTAAGAGCCAGGTAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGA
GTTTGTCTCAAAGTTTTCGGATATCAATGACAATGAACCAAAATCTTCAGATGAACCTTATG
AGGCCATTGTACAGAGATGTCTCCAGGAAGCAATAGTATTACAGGTGACAGCAAGTGA
GCTGCAGCATCCCTCAAGTGGTAAATAGTCTGCTCTCTCTACAGCTTACTTCAAGGCCAGCC
ATATTTTCTGTGAACCAACAGGAGTCAAGAATATCTTTAAATGGGATAGAGGAGT
TGCAAGATGAGTATTGGGTAATCATTCAGCCCAAGGACATGATTGGTCAGCCAGCAGGCTTG
TCTGGAAACAAGGTGTAATTAATTAACCTTTAGATGTTATGACAATAAGCCTATATTATTA
AGAAAGTTTATCCCGTGACTGTCTGAAATCTGCACCCTGGGACTTCTATAGGAACAA
TCATGGCATATGATAATGACATAGGAGAGAAATGCAGAAATGGATTACAGCATTTGAAGAGAT
GATTCGCAACCAATTTGACATTTACTTAATCATGAAACTCAAGAGGAATAGTTTATATTAA
AAGAAAGTGGATTTTGGACACAGAACCACTACGGTATTAGAGCAAAAGTTAAAAACCATC
ATGTTCTCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCACCTTTCATTAAAGATCCAG
GTGGAAGATGTTGATGAGCCTCCTCTTTTCTGCTTCATATATGTTATGTTTGAAGTTTGTGA
AGAAACCCACAGGAGTCAATTTAGCCGCTGGTGTCTGCACAGAACCCAGACAATAGGAAAT
CTCCTATACGGTAATCTATTACTAGGAGCAAAGTGTCCAATATCAATGATAATGGTACAATC
ACTACAAGTACTCACTGGATCGTGAATCAGTGTCTTGGTACAACCTAGTATTACAGGCCAC
AGAAAAATACAATATAGAACAGCTCTTCCTGATCCCATGTATGTCAAGTTCTTCAACATCA
ATGATCATGCTCTGAGATTTCTCTCAATACATATAGACATATGTTTGTGAAAATCGAGGCTCT
GTGCAGGTAACTGACAGTATCAGTGTGAGTGTAGATAGATGAATCCATAGAGAAGCACCATT
TTACTTTAAICTATCTGTAGAAGACCTAACAAITCAAGTTTACAATCATAGATAATCAAG
ATAACACAGCGTGTCAATTTGACTAATAGAAGCTGTTTAACTTCAAGAAGAACCTGTCTTC
TACATCTCCATCTTAATTTGCGCAATGGAATCCCGTCACTTACAAGTACAAACCCCTTAC
CATCCATGCTGTGACTGTGTGTCAGAGTGGGAGCACACAGACCTGCCAGTACCAGAGCTTG
TGCTTTCCATGGATTCAAGACAGAAGTTATCATTTGCTATTCTCATTTTGATTATGATCATAT
TTTGGGTTTATTTTTCGACTTTGGGTTTAAACCAACGGAGAAAACAGATTCTATTCTCTGA
GAAAAGTGAAGATTTCAGAGAGAATATATTCCAATGATGATGAAGGGGTGGAGAAGAAG
ATACAGAGGCGCTTGATATGACAGAGCTGAGGAGTAGTACCATAATGTGGGGGAACGAGAGCT
CGGAAAACCAAGCGCTGAGATCAGGAGCCTATACAGGCAAGCTTTGCAAGTTGGCCCCCGA
CAGTGCCATATTTCAGGAATCTCATCTGGAAGAGCTCGAAGAGCTTAATCTGATCCGTTGT
CCCCCTTTTGTATTCCTCTCAGACTTACGCTTTTGGGGAAACAGGCTCATTAGCTGGATCC
CTGAGCTCTCTAGAATCAGCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTT
GGGACCTCGCTTTAAAGATTAGCATGCTATTTGGTTCTGACGTGACGTAATATTAAGT
GCTTTTACCATCAAAATTTTAAAGTGCTAAATGTGATTGCAACCAATGGTGTAGTCTTAA
AGAGTTTGTGCGCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTTCTGATTTCC
CTGGAGTAAATATCCATGGTTTATTTTAAGCTACCTACATCGTGTATTGGAACAGAGATGTG
GGGAGAAATGTAAACCATCGCTCAGCGCATCAATACACCGAGATTGGAAGTAAAAATATG
TAGGAGAGATATTAAGAGGTAGATGAGAGGACACAAGATGTAGTCTGATCCTTATGCGATTATAT
CATTTATTTACTTAGGAAAGTAAAAATACCAACGAGAAAAATTTAAAGGAGCAAAAAATTTG
CAAGTCAATAGAAATGTACAAATCGAGATAACATTTACATTTCTATCATATTGACATGAA
ATTGAAAATGTATAGTCAGAGAAATTTTCATGAATATTTCATGAAGTATTGTTTCTTTAT
TTAA

FIGURE 95

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906

><subunit 1 of 1, 772 aa, 1 stop

><MW: 87002, pI: 4.64, NX(S/T): 8

MNCYLLLRFMLGIPLLWPCLGATENSQTKKVKQPVRSHLRVKRGWVWNQFFVPEEMNTTSHH
IGQLRSDLNDGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT
GRAVEPESEFVIKVS DINDNEPKFLDEPYEAIVPEMSPECTLVIQVTASDADDPSSGNNARL
LYSL LQGQPYFSVEPTTG VIRISSKMDRELQDEYVWIIQAKDMIGQPGALSGTTSVLIKLSD
VNDNKPIFKESLYRLTVSESAPTGTSGITIMAYDNDIGENAEMDYSIEEDDSQTFDIIITNHE
TQEGIVILKKKVD FEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFL
PYVFEVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISA
WYNSITATEKYNIEQISSIPLYVQVLNINDHAPFSQYYETVVCENAGSGQVIQTISAVDR
DESI EHHFYFNLSVEDTNNSSTFIIDNQDNTAVILTNRTGFNLQEEP VFYISIL IADNGIP
SLTSTNTLTIHVCDGDSGSTQTQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTLGLKQ
RRKQILFPEKSEDFRENI FQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLY
RQSLQVGPDS AIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGLAGSLSSLESASVDQD
ESYDYLNELGPRFKRLACMFGSAVQSNN

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 597-617

N-glycosylation sites.

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,
516-519 and 534-537

Cadherins extracellular repeated domain signature.

amino acids 136-146 and 244-254

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FIGURE 96

ATTTC AAGCCAGCCATATTTTNTGTTGAACCAACAACAGGAGTCATAAGAATATTTNTA
AAATGGATAGAGAACTGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGT
CAGCCAGGAGCGTTGNTGGAACAACAAGTGTATTAATTAACTTTCAGATGTTAATGACAA
TAAGCCTATATTTAAAGAAAGTTTATACCGCTTGACTGTNTNTGAATCTGCACCCACTGGGA
NTTNTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTAC
AGCATTGAAGAGGATGATTCGCAAACATTGACATTATT

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FIGURE 97

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCGCGCCCGGGCGCGGACCCCAACCCCGAC
CCAGAGCTTCTCCAGCGCGCGCGCAGCGAGCAGGGCTCCCCGCCCTTAACTTCCTCCGCGGGG
CCCAGCCACCTTCCGGGAGTCCGGGTGCGCCACCTGCAAACTCTCGCGCTTCTGACACCTGCCA
CCCTCGAGCCAGCGCGGGCCCCGAGCGAGT**CATGG**CCAACGCGGGGCTGCAGCTGTTGGGC
TTCATTCTCGCCTTCTCGGATGGATCGGCGCCATCGTCAGCACTGCCCTGCCCCAGTGGAG
GATTTACTCCTATGCCGCGCAACAACATCGTGACCGCCAGGCCATGTACGAGGGGCTGTGGA
TGTCTCTGCGTGTGCGCAGAGCACCGGCGAGATCCAGTGCAAAAGTCTTTGACTCCTTGCTGAAT
CTGAGCAGCACATGTCAAGCAACCGTGCCCTTGATGGTGGTGGCATCTCTCGGAGTGAT
AGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGAAGACGATGAGGTGC
AGAAGATGAGGATGGCTGTCAATGGGGGTGCGATATTTCTTCTTGCAAGTCTGGCTATTTTA
GTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATCTATGACCCCTATGACCCCGAT
CAATGCCAGGTACGAATTTGGTCAAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCGCC
TTCTGGGAGGTGCCCTACTTTTGTCTGTCTCTGTCGCCGAAAAACAACCTCTTACCCAAACCA
AGGCCCTATCCAAAACCTGCACCTTCCAGCGGGAAGACTACGT**GTG**CACAGAGGCAAAAG
GAGAAAAATCATGTTGAACAACCGAAAAATGGACATTGAGATACATCTAATTAACATTAGGAC
TCTAGAATTTTGGGTATTGTAATCTGAAGTATGGTATACAAAAACAAACAAACAAAA
ACCCATGTGTTAAAAATACTCAGTGCTAAACATGGCTTAATCTTATTTTATCTTCTTCTCA
ATATAGGAGGGAGATTTTCCATTGTATTACTGCTTCCATTGAGTAATCATACTCAAT
GGGGGAGGGGTGCTCTTAAATATATATAGATATGTATATACATGTTTTCTATTAAAA
ATAGACAGTAAAAATACTATTCTCATTATGTTGATACATAGCATACTTAAATATCTCTAAAT
AGGTAATGTATTTAATTCATATTGATGAAGATGTTTATTTGGTATATTTCTTTTTCTGCTC
TTATATACATATGTAACAGTCAAAATATCATTTACTCTTCTCATTAGCTTTGGGTGCTTTG
CCACAAGACCTAGCCTAATTTACCAAGGATGAATCTTTCAAATCTTCACTGCGTGCCCTTT
CATATACTTATTTTATTTTTTACCATAATCTTATAGCACTTGCACTGTTATTAAGCCCTTT
TGTGTTTTGTGTTTCATTGGTCTCTATCTCTGAAATCTAACACATTTCTATAGCTACATTTTA
GTTTCTAAAGCCAAGAAGATTTATTACAAATCAGAACTTTGGAGGCAAACTCTTCTGCAATG
ACCAAAGTGATAAATTCCTGTGACCTTCCACACAATCCCTGTAATCTGACCCATAGCACT
CTTGTTTGCTTTGAAAAATATTGTCCAATTGAGTAGCTGCATGCTGTTCCCCCAGGTGTTGT
AACCAACCTTATTGTATTGAATTTTTTAAGCTACTTATTCATAGTTTTATATCCCCCTAACT
ACCTTTTTGTTCCTTCTTAATTTGTATTGTTTTTCCCAAGTGTAATTATCATGCGTTTTA
TATCTTCTAATAAGGTGTGGTCTGTTTGTCTGAACAAAGTGCTAGACTTTCTGGAGTGATA
ATCTGGTGACAAATATTCTCTGTAGCTGTAAGCAAGTCACTTAATCTTTCTACCTCTTT
TTCTATCTGCCAAATGAGATAATGATACTTAACCAAGTTAGAAGAGGTAGTGTGAATATTA
TTAGTTTATATTACTCTTATTCTTTGAACATGAACATATGCCTATGTAGTGTCTTTATTTGCT
CAGCTGGCTGAGACACTGAAGAAGTCACTGAACAAACCTACACACGTACCTTCATGTGATT
CACTGCCCTTCTCTCTACAGTCTATTCCACTGAACAAAACCTACACACATACCTTCAT
GTGGTTCAGTCCCTTCTCTCTCTACCAGTCTATTTCCACTGAACAAAACCTACGCAATAC
CTTCATGTGGCTCAGTGCCCTTCTCTCTCTACCAGTCTATTTCCATCTTTCCAGCTGTGTGCT
GACATGTTTGTGCTCTGTTCATTTTAAACAATGCTCTTACTTTTCCAGTCTGTACAGAATG
CTATTTCACTTGACAGAGATGATGTAATGGAAGGGTGTGGCACTGGTGTCTGGAAGCTG
GATTTGAGTCTTGGTGTCTATCAATCACCGTCTGTGTTTGAGCAAGGCATTTGGCTGCTGTAA
GCTTATTGCTTCATCTGTAAGCGGTGTTTGTAAATCCTGATCTTCCACCTCACAGTGATG
TTGTGGGGATCCAGTGAGATAGAATACATGTAAGTGTGGTTTTGTAATTTAAAAAGTGCTAT
ACTAAGGGAAAGAAATGAGGAATTAACATGCATACGTTTTTGGTGTGCTTTTCAAATGTTTGA
AAATAAAAAAATGTTAAG

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FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185
><subunit 1 of 1, 211 aa, 1 stop
><MW: 22744, pI: 8.51, NX(S/T): 1
MANAGLQLLGFI LAFLGWIGAIVSTALPQWRIYSYAGDNIVTAQAMYEGLMWSCVVSQSTGQI
QCKVFDSLNLNLSSTLQATRALMVVGILLGVIAIFVATVGMKCMKCLEDEDEVQMRMAVIGGA
IFLLAGLAILVATAWYGNRIVQEFYDPMTPVNNARYEFGQALFTGWAAASLCLLGGALLCCSC
PRKTTSYPTPRPYPKPAPSSGKDYV

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-102, 118-142 and 161-187

N-glycosylation site.

amino acids 72-75

PMP-22 / EMP / MP20 family proteins

amino acids 70-111

ABC-2 type transport system integral membrane protein

amino acids 119-133

FIGURE 99

TTCTGGCCAAACCCGGGGCTNCAGCTGTTGGGCTTCATCTCGCCTTCCTGGGATGGATCGGC
GCCATCNTCACACTGCCCTTCCCCAGTGGAGGATTTTACTCCCTATGCTGGCGACAACATCG
TGACCGCCCGAGCCCATGTACGAGGGGCTGTGGATGTCCNGCGTGTGCAGAGCACCGGGCAG
ATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCCGTGC
CTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGA
AGTGTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGC
GCGATATTTCTTCTTGAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAAN
CNTTCAACANTTCTATGACCCTATGACCCAGTCAATGC CAGGTACGAATTTGGTCA
GGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCTTCTGGGAGGTGCCCTACTTTGCT
GTTCCCTGTCCC

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FIGURE 100

ACCCTTGACCCAACGCGGCCCGACCGNTTCATGGCCAAACGCGGGNCTCCAGCTGTTGG
GCTTCATTCTCCCTTCCTGGGATGGACCGGCGCCCATCNTCAGCACTGCCCTGCCCCAGTG
GAGGATTACTCCTATNCCGGCNACAACATCGTGACCGCCAGGCCNTGTACGAGGGGCTGT
GGATGTCCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCCTTGCT
GAATCTGAGCAGCACATTGCAAGCAACCCGTGCCCTTGATGGTGGTTGGCATCCTCCTGGGAG
TGATAGCAATCTTNNTGGCCACCGTGTGTTNNNTGAAGTGTATGAAGTGCTTGAAGACGATGA
GGTGCAAGATGAGGATGGCTGTCAATTGGGGCGGATATTTCTTCTTGAGGTCTGGCTA
TTTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCGA

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FIGURE 101

GGGCCCACCATTATCCAACCGGGNTCACTGTTGGCTCATCTCCCTCCTGGATGAANCGCGC
CATCNTCAGACTCCCTGCCCCATGGAGATTNNCCTATGCTGGCGACAACATCNTGACCCCC
AGCCATGTACGAGGGGCTTTGAACGTCNGCGTGTGCGAGANCAACGGGCAGATCCAGTGCAA
AGTCTTTGACTCCTTGCTGAATCTGNGCAGCACATTGCAGCAACCCNTGCCCTGATGGTGGT
TGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGT
GCTTGGAAGACGATGAGGTGCAGAAAGATGAGGATGGCTGTCAATTGGGGGCGCGATATTTCTT
CTTGCAAGTCTGGCTATTTNNNGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAAT
TCTATGACCCTATGACCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGC
TGGGCTGCTGCTTCTCTGCTTCTGGGAGGTGCCCTACTTTGCTGTTCTCTGCGA

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FIGURE 102

ATTCTCCCCTCCTGGATGGATCGCNCCACCGTCACATTGCCTTCCCCCANTGGAGGATTNAC
TCCTATGCTGGCGACAACATCGTGACCCCCCAGGCCATTTACCGAGGGGCTTTGGATGTCNT
GCNTGTCGCAGAGCACCGGGCAGATCCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAG
CAGCACATTGCAAGCAACCCGTGCCCTTGATGGGGTTGGCATCCTCCTGGGAGTGATAGCAAC
CTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGAAGACGATGAGGTGCCAGAAG
ATGAGGATGGCTGTCAATTGGGGGCGCGATATTTCTTGTTGCAGGTCTGGCTATTTTAGTNGC
CACAGCATGGTATGGCAATAGANTNNTTCNNGNNNTCTATGACCCTATGACCCCAAGTCAATG
CCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCTTCTG
GGAGGTGCCCTACTTTGCTGTTCTGTGCC

109101-4958/560

FIGURE 103

AGAGCACCGGCAGATCCCAGTNCAAAGTCTTTGACCCTTGCTGAATCTGAGCAGCACATTNC
AAGCAACCCCTTGCCTTGAAGGTGGTTGNCATCCCCCTGGGAGTGAATAGCAATCTTTGTG
GCCACCGTTGGCATGAAGTNTATGAAGTGCTTGAAGACGATGAGGTGCAGAAGATGAGGAT
GGCTGTCAATGGGGGCGCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGTNNCCACAGCAT
GGTATGGCAATAGNATNNTTCGNGGNTTCTATGACCCTATGACCCAGTCAATGCCAGGTAC
GAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGTCCTTCTGGGAGGTGC
CCTACTTTGCTGTTCTCTGTCCCCGAA

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FIGURE 104

AGCAATGCCCTGCCCCAGTGGAGGATTAATTCCTATGNTGGGGACAACATTGTGACNGCCC
AGGCCATGTACGGGGGGCTGTGGATGTCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGC
AAAGTNTTTGACTCCTTGCTGAATTTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGT
GGTTGGCATCTTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTGGNAATGAAGTGATGA
AGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTT
CTTNTTGCAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAAATNGTTCAGA
ATTTTATGACCCATATGACCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTTTNTTCACTG
GCTGGGCTGCTGCTTNTTCTGCCTTNTGGGAGGTGCCTANTTTGCTGTTCTGCGAACC

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FIGURE 105

TCATAGGGGGCGCGATATTTTTCTTGCAGGTNTGGTTATTTTAGTTGCCACAGCATGGTA
TGGCAATAGAATCGTTCAAGAATTNTATGACCCCTATGACCCCAAGTCAATGCCAGGTACGAAT
TTGGTCAGGCTCTNTTCACTGGNTGGGCTGCTGCTTCTNTNNGCCTTNTGGGAGGTGCCCTA
CTTGCTGTTCCCTG

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FIGURE 106

TTCTCTGGGATGGATCCGCCCCCATCNTCACATGCCCTGCCCCNTGGAGATTTACNCCTATGC
TGGCGAACAACATCNTGACCGCCAGGCCATGTACGAGGGGCTGTGGAATGTCCTGCGTGTCTC
CCAGAGCACCGGGCAGATCCAGTGC AAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACAT
TGCAAGCAACCNTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGG
CCACCGTTGGCATGAAAGTGTATGAAGTGCTTGAAGACGATGAGGTGCAGAAGATGAGGAT
GGCTGTCATTGGGGGCGCATATTTCTTCTTGCAAGTCTGGCTATTTTAGNNGCCACAGCAT
GGTATGGCAATCAGACCCNNTCANAACTCTATGACCCATGACCCAGTCAATGCCAGGTA
CGAATTTGGTCAAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTG
CCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCACG

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FIGURE 107

CGGGGCTGCAGCTGTTGGGCTTCATCTCGCTTCCTGGGATGGAATCGGGGCCATCGTCAGCA
CTGCCCTGCCCCATGGAGGATTTACTCNTATGCTGGCGACAACATCGTGACCNCCCAGGCCA
TGTACGAGGGGCTGTGGATGTCNGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCT
TTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCNTGCCTTGATGGTGGTTGGCA
TCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCCTG
GAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCAATTGGGGGCGCGATATTTCTTCTTGC
AGGTCTGGCTATTTNTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTAT
GACCCATGACCCAGTCAATGCCAGGTACGAATTTGGTCAAGGCTCTCTTCACTGGCTGGGC
TGCTGCTTCTCTCTGCTTCTGGGAGGTGCCCTACTTTGCTGTTCTTCGCGAA

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FIGURE 108

CGGTGCCGTGCTCGCGGGGACCGCGGGCTCGCCCTCGCCCTCGGCCCTGCGCCCTGCAC
 CGGTAGACCGACCCCCCTCCAGCGCGCCACCCGGTAGAGGACCCCGCCCGTGCCTCG
 ACCGGTCCCGCCTTTTGTAAAACTTAAAGCGGGCGAGCATTACGCTTCCGCCCCGGT
 GACCTCTCAGGGGTCTCCCCGCCAAGGTGCTCGCGCGCTAAGGAACATGCGCGAAGGTGGAG
 CAGGTCTGAGCCTCGAGCCGCGAGCAGAGCTCAAATTCGAGGTCCTTCACCGATGTTGT
 CACCACCAACCTAAAGCTTGGCAACCCGACAGACCGAAATGTGTGTTTAAAGGTGAAGACTA
 CAGCACCACGTAGGTACTGTGTGAGGCCAACAGCGGAATCATCGATGAGGGGCCCTCAAT
 AATGTATCTGTGATGTTTACAGCCTTTCGATTATGATCCCAATGAGAAAAAGTAAACACAAGT
 TATGTTTCACTCTATGTTTGTCTCCAATGACACTTCAGATATGGAAGCAGTATGGAAGGAGG
 CAAAACCGGAAGACCTTATGGATTCAAACTTAGATGTGTGTTGAATTGCCAGCAGAGAAT
 GATAAACCATGATGTAGAAAATAATAAAATTATATCCACAACATGCATCAAAGACAGAAAC
 ACCAATAGTGTCTAAGTCTCTGAGTCTCTTTGGATGACACCGAAGTTAAGAAGGTTATGG
 AAGAATGTAAGAGGCTGCAAGGTGAAGTTGAGAGGCTACGGGAGGAGAACAGCAGTTCAAG
 GAAGAAGATGGACTGCGGATGAGGAAGACAGTGCAGAGCAACAGCCCCATTTAGCATTAGC
 CCAACTGGGAAGGAAGAAGGCCCTTAGCACCCGGCTCTGGCTCTGGTGGTTTGTCTTTA
 TCGTTGGTGAATTTATTGGGAAGATTGCCCTGTAGAGGTAGCATGCACAGGATGGTAAATTG
 GATTGGTGGATCCACCATATCATGGGATTTAAATTTATCATAACCATGTGTAAGAAAGAAAT
 AATGTATGATGACATCTCACAGGTCTTGCCTTTAAATTTACCCCTCCCTGCACACACATACAC
 AGATACACACACAAAATAATGTAACGATCTTTTAGAAAAGTTAAAAATGTATAGTAACTG
 ATTGAGGGGGAAAAAGATGATCTTTATTAATGACAAGGGAACCATGAGTAATGCCACAAT
 GGCATATTGTAATGTCAATTTAAACATTGGTAGGCCTTGGTACATGATGCTGGATTACCTC
 TCTTAAATGACACCCCTTCCCTCGCTGTTGGTGTGGCCCTTGGGGAGCTGGAGCCAGCAT
 GCTGGGGAGTGGGTGAGCTCCACACAGTAGTCCCCAGTGGGCCACTCCCGGCCAGGCTG
 CTTTCGGTGTCTTCACTCTGTCCAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGA
 AGCCCAAAGGAATGCACTGTGGCAGCATCAGAGCTACTCGTCATAAGTGAGAGGCGTGTGT
 TGACTGATTGACCCAGCGCTTTGGAATAAATGGCAGTGCTTTGTTCACCTTAAAGGGACCAA
 GCTAAATTTGATTGGTTCATGTAGTGAAGTCAAACGTATTTCAGAGATGTTTAAATGCATA
 TTTAACTTATTTAATGTATTTTATCTCATGTTTCTTATTGTGACAAGAGTACAGTTAATGC
 TCGCTGTCTGCTGAACCTGTGTTGGGTGAACGTGATTGCTGCTGGAGGGCTGTGGGGCTCCTCT
 GTCTCTGGAGAGTCTGGTCATGTGGAGGTGGGGTTTATTGGGATGCTGGAGAAGAGCTGCCA
 GGAAGTGTTTTCTGGGTGAGTAAATAACAACCTGTATAGGAGGGGAAATTCAGTAGTG
 ACAGTCAACTTAGGTTACCTTTTAAATGAAGAGTAGTCAGTCTTCATGATTGTTCTTATA
 CCACCTCTCAACCTATTCTCACACTCCAGCGCCAGGTCCAAGTCTGAGCCTGACCTCCCC
 TTGGGGACCTAGCCTGGAGTCAGGACAATGGATCGGGCTGCAGAGGGTTAGAAGCGAGGGC
 ACCAGCAGTTGTGGTGGGGAGCAAGGGGAAGAGAGAAACTCTTCAGCGAATCCTTCTAGTAC
 TAGTTGAGAGTTTACTGTGAATTAATTTTATGCCATAAAAGACCAACCCAGTTCTGTTTGA
 CTATGTAGCATCTTGAAGAAAAAATTATAATAAAGCCCCAAATTAAGAAAA

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<subunit 1 of 1, 243 aa, 1 stop

MAKVEQVLSLEPQHEHLKFRGPFPTDVVTNLKLGNPTRDNRVCFVKVTTAPRRYCVRPNSGIID
AGASINVSVMLQPFDYDPNEKSKHKFMVQSMFAPTDTSDMEAVWKEAKPEDLMDSKLRVFE
LPAENDKPHDVEINKIIISTTASTKTETPIVSKSLSSSLDDTEVKVMEECKRLQGEVQRLREE
NKQFKEEDGLMRKTVQSNSPIALAPTKEEGLSTRLLALVVLFFIVGVIIGKIAL

Important features:

Transmembrane domain:

amino acids 224-239

N-glycosylation site.

amino acids 68-71

N-myristoylation site.

amino acids 59-64, 64-69 and 235-240

FIGURE 110

GTCAGTCTTCTAGATTGTCCTTATCCCACCTTTCAACCANTACTCACATTTTCNAGCGCCCAG
GTCCANGTCTGAGCCTGACTTCCCCTTGGGGACCTAGCCTGGAGTCAGGACAATGGNTCGGG
CTGCAGAGGNTTAGAAGCGAGGGCACCAGCAGTTTTGGGTGGGGAGCAAGGGNNGAGAGAAA
CTCTTCAGCGAATCCTTCTAGTACTAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATA
AAAGACNAACCCAGTTCTGTTTGACTATGTAGCATCTGAAAAGAAAAATTATAATAAGCC
CCAAAATTAAGAATTCTTTTGTCAATTTGTACATTTGCTCTATGGGGGAATTATTATTTT
ATCATTTTATTATTTTGGCCATTGGAAGGTAACTTTAAATGAGC

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FIGURE 111

TATTGTAAAGGCCATTTTAAACCATTGGTAGGCCTTGGTACATGATGCTGGATTACCTCCTT
AAATGACACCNNTTCCTCGCCTGTTGGTGCTGGCCNNTGGGGAGCTGGAGCCCCAGCATGCTG
GGGAGTGC GGTCAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCCAGGCTGCTTT
CCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCC
CAAAGGAATTGCCACTGTGGCAGCATCAGACGTA CTGTCATAAGTGAGAGGCGTGTGTTGA
CTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAAGCT
AAATTGTATTGGTTCATGTAGTGAAGTCAAAC TGTTATTCAGAGATGTTTAATGCATATTTA
ACTTATTTAATGTATTT CATCTCATGTTTTCTTATTGT CACAAGAGTACAGTTAATGCTGCG
TGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTG

109101-1958/560

FIGURE 112

CCCTGGTGGTTTTGTTCTTTAATTCGTTGGTGTAAATNTTGGGAAGATTGCTTGTAGAGGTA
GNATGCACCNGGCTGGTAAATTGGATTGGTGGATCCACCATATCCATGGGATTTAAATTTAT
CATAACCATGTGTAAAAAGAAATTAATGTATGATGACATNTCACAGGTATTGCCTTTAAATT
ACCCATCCCTGNANACACATACACAGATACACANANACAAATNTAATGTAACGATNTTTTAG
AAAGTTAAAAATGTATAGTAAC

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109101.4958/660

FIGURE 113

GGTGGCCCATTCCTGGCCAGGCTGCTTTCCGGTNTTCAGTTCTGTCCAAGCCATCAGCTCC
TTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATNAGACGTAC
TTGTNATAAGTGAGAGGCGTGTGTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGT
GCTTTGTTTCANTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACG
TTATTCAGAGATGTTTAAATGCATATTTAANTTATTTAATGTATTNATNTCATGTTTCTTA
TTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAANTNTGTTGGGTGAACTGGTATTGC
TGCTGGAGGGCTGTGGGCTCCTCTGTCTTTGGAGAGTCTGGTCATGTGGAGGTGGG

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FIGURE 114

TGCTTTCCGTGTTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTTGATGAACAGAGTC
AGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTG
TGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGAC
CAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACCTGTTATTCAGAGATGTTTAATGC
ATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAA
TGCTGCGTGC

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FIGURE 115

AAACCTTTAAAAGTTGAGGGGAAAAGAATGATCCTTTATTAATGACAAGGGAAACNTGNGT
AATGCCACAATGGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGC
TGGATTACCTCTCTTAAATGACACCCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTN
GAGCCCAGCATGCTGGGGAGTGCGGTCTGCTCCACACAGTAGTCCCCANGTGGCCANTCCC
GGCCCAGGCTGCTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGANTGATGA
ACAGAGTCAGAAGCCCAAAGGAATGCAANTGTGGCAGCATCAGANGTANTNGTCATAAGTGA
GAGGCGTGTGTTGANTGATTGACCCAGCGCTTGGGAAATAAATGGCAGTGCTTTGTTCAANTT
AAAGGGNCCAAGNTAAATTTGTATTGGTTCATGTAGTGAAGTCAAANTGTTATTTCAGAGATG
TTTAATGCATATTTAANTTATTTAATGTATTTCAATNTCATGTTTTCTTATTGTCAAGGGT
ACAGTTAATGCTGCGTCTGCTGAANTCTGTTGGGTGAANTGGTATTGCTG

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FIGURE 116

GGCCCTTGGGGAGCTGGAGCCCAGCATGCTGGGGAGTGCGGTCAGCTCCACACAGTAGTCCC
CACGTGGCCCACTCCCGGCCAGGCTGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGC
TCCTTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACG
TACTCGTCATAAGTGAGAGGCGTGTGTGACTGATTGACCCAGCGCTTTGGAAATAAATGGC
AGTGCTTTGTTCACTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAA
CTGTTATTCAGAGATGTTTAATGCATATTTAACTTATTTAATGTATTTTCATCTCATGTTTT
TTATTGTACAAGAGTACAGTTAATGCTGCGTGCTGCTGAACTCTGTTGGGTGAACTGGTAT
TGCTGCTGGAGGGCTGTGGGCTCCTCTGTCTCTGGAGAGTCTGGTCATGTGGAGGTGGG

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FIGURE 117

GCAGACTCCGGGTGCTGTGGCCCCGGCCTTGGCGGGGGCGGCTCCGGCTCAGGCTGGCTGAGA
GGCTCCCAGCTGCAGCGTCCCCGCCCGCCTCCTCGGAGACTCTGATCTCAGCTGCAGTGGC
CTCGGGGACCAACAAGCCTGGCAGGGTCTCACTTTGTTGCCAGGCTGGAGTTTCAGTGCCA
TGATCATGTTTACTGCGACCTTGACCTCCTGGGTTCAGCGATCCTGCTGAGTAGCTGGGA
CTACAGGACAAAATTAGAAGATCAAAATGGAAAATATGCTGCTTTGGTTGATATTTTTCACC
CCTGGGTGGACCCCTCATTTGATGGATCTGAAATGGAAATGGGATTTTATGTGGCACTTGAGAAA
GGTACCCCGGATTGTTCAGTGAAGGACTTTCATCTCACCAGCCCCGATTTCAGGCGAGATG
CTAAGATGATGGTAAATACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCAACTCCCAGC
CTTTCTGAATTGGAGGATTTATCTTTCTATGAGACTGTCTTTGAGAATGGCACCCGAACTTT
AACCAGGGTGAAGTTTCAAGATTTGGTTCTTGAGCCGACTCAAAATATCACCACAAAGGGAG
TATCTGTTTAGGAGAAAGAGACAGGTGTATGGCACCGACAGCAGGTTTCAGCATCTTGGACAAA
AGGTTCTTAACCAATTTCCCTTTTCAGCACAGCTGTGAAGCTTTCCACGGGCTGTAGTGGCAT
TCTCATTTCCCCTCAGCATGTTCTAACTGCTGCCACTGTGTTTCATGATGGAAGGACTATG
TCAAAGGGAGTAAAAAGCTAAGGGTAGGGTTGTTGAAGATGAGGAATAAAAGTTGGAGGCAAG
AAACGCTCGAGGTTCTAAGAGGAGCAGGAGAGAAGCTAGTGGTGGTGACCAAAGAGAGGGTAC
CAGAGAGCATCTGCAGAGAGAGAGCGAAGGGTGGGAGAAGAAGAAAAAATCTGGCCCGGGTCT
AGAGGATTGCCGAAGGGAGGCTTCTCTTTCAGTGGACCCGGGTCAAGAATACCCACATTTCCG
AAGGGCTGGGCAAGAGGAGCATGGGGGACGCTACCTTGGACTATGACTATGCTCTTCTGGA
GCTGAAGCGTGCTCACAAAAAGAAATACATGGAACCTTGAATCAGCCCAACCGATCAAGAAAA
TGCCTGGTGAATGATCCACTTCTCAGGATTTGATAACGATAGGGCTGATCAGTTGGTCTAT
CGGTTTTGCAGTGTGTCCGACGAATCCAATGATCTCCTTTACCAATACCTGCGATGCTGAGTC
GGGCTCCACCGGTTTCGGGGGTCTATCTGCGTCTGAAGAATCCAGACAAAAAGAATTGGAAGC
GCAAAATCATTTGGGCTTACTCAGGGCACCAGTGGGTGGATGTCACCGGGGTTTCAGAAGGAC
TACAACGTTGCTGTTTCGCATCACTCCCTTAAAAATACGCCCAAGTTTCCTCTGGATTACGG
GAACGATGCCAATTTGTGCTTACGGCTTAAACAGAGACCTGAACAGGGCGGTGTATCATCTAAA
TCACAGAGAAAAACAGCTCTGCTTACCGTAGTGAGATCACTTCATAGGTTATGCCCTGGACTT
GAACCTGTCAATAGCATTTCAACATTTTCAAATCAGGAGATTTTCGTCATTTAAAAAA
TGTATAGGTGCAGATATTGAAACTAGGTGGGCACTTCAATGCCAAGTATATACTCTTCTTTA
CATGTTGATGAGTTTCATTTGTAGAAAAATTTTGTGCTTCTTAAAAATTAGACACACTTT
AAACCTTCAAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATTTCTCAGGGTCC
TACTCTAAGAAGAACTTAATAGGATGCTGGTTGTGTATTAATGTGAATTTGCATAGATAAA
GGTAGATGGTAAAGCAATTAGTATCAGAATAGAGACAGAAAGTTTACAACAGCTTTGTACTA
CTCTGAGATGGATCCATTCAGCTCATGCCCTCAATGTTTATATTGTGTTATCTGTTGGGTCT
GGGACATTTAGTTTATGTTTTTTGAAGAATTACAAATCAGAAGAAAAAGCAAGCATTATATAAA
CAAACTATAACTGTTTCTGCTTTTAAAGAAATAACAAATACATGTGTATTTATTTAAAAA
TGGGAGAAATAGTTTGTCTATGAAATAAACCTAGTTTAGAAATAGGGAAGCTGAGACATTT
TAAGATCTCAAGTTTTTATTTAACTAATACTCAAAATATGGACTTTTCATGTATGCATAGGG
AAGACACTTCACAAATATGAATGATCATGTGTGTGAAGCCACATATTTTATGCTATACAT
TCTATGTATGAGGTGCTACATTTTGAAGCAAGAAATTTCTGTAATCTTTTCAAGAAAGAGT
CTTTTCTCCTTGACAAATCCAGCTTTTGTATGAGGACTATAGGTGAATTTCTGATTAG
TAATTTTATAGATATGCTCTTCTTCTAAAAATGAATAAAATTTATGAATATGA

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FIGURE 118

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253
<subunit 1 of 1, 413 aa, 1 stop
<MW: 47070, pI: 9.92, NX(S/T): 3
MENMLLWLIFFTPGWTLLIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAPEADAKMMVNTVC
GIECQKELPTPSLSELEDYLSYETVFENGTRTLTRVKVQDLVLEPTQNITTKGVSVRRKRQV
YGTDSRFSIILDKRFLTTFPFSTAVKLSTGCSGILISQHVLTAAHCVHDGKDYVKGSKKLRV
GLLMRNKSGGKKRRGSKRSRREASGGDQREGTREHLQERAKGRRRKSGRGQRIAEGRPS
FQWTRVKNTHIPKGWARGMGDATLDYDYALLELKRAHKKKYMELGISPTIKKMPGGMIHFS
GFDNDRADQLVYRFCVSVDESNDLLYQYCDAESGSTGSGVYLRKDPDKKNWKRKIIVYSG
HQWVDVHGVQKDYNNVAVRITPLKYAQICLWIHGNDANCAYG

Important features:

Signal peptide:

amino acids 1-16

N-glycosylation sites.

amino acids 90-93, 110-113 and 193-196

Glycosaminoglycan attachment site.

amino acids 236-239

Serine proteases, trypsin family, histidine active site.

amino acids 165-170

00070564-101601

FIGURE 119

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTAGCACCAGTACTGGAT
GTGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTAGTGTCCGATTCTGATTCGGCAAGG
ATCCAAGCATGGAATGCTGCCGTGGGCAACTCTGGCACACTGCTCCTCTTTCTGGCTTTC
CTGCTCCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGACGGCCTATGGGATGCGCTG
GGGCCCATGGAGTGAATGCTCACGCACCTGCGGGGGAGGGGCTCCTACTCTCTGAGGCGCT
GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC
TGCCACCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA
CCATGGCCAGTTTTATGAATGGCTTCTCTGTGTCTAATGACCCTGACAACCCATGTTCACTCA
AGTGCCAAAGCCAAAGGAACAACCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACG
CGTTGCTATACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTGTTGGCTGCGA
TCACCAGCTGGGAAGCACCCGTCAAGGAAGATAACTGTGGGGCTGCAACCGGAGATGGGTCCA
CCTGCCGGCTGGTCCGAGGGCAGTATAAATCCAGCTCTCCGCAACCAATCGGATGATACT
GTGGTTGCACTTCCCTATGGGAAGTAGACATATTGCGCTTGTCTTAAAGGTCTCGATCACTT
ATATCTGGAACCAAAACCCCTCCAGGGGACTAAAGGTGAAAAACAGTCTCAGTCCACAGGAA
CTTTCTTGTGGACAATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGA
ATGGCTGGACCACTCACAGCAGATTTCAATTGTCAAGATTTCGTAACCTCGGGCTCCGCTGACAG
TACAGTCCAGTTCATCTTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTC
CTTGCTCAGCAACCTGTGGAGGAGGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGG
AGCAACCGTGTGGTTGCTGACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACC
CAAGCTTCAGGAGTGCAACTTGGATCCTGTGCCAGCCAGTGACGGATACAAGCAGATCATGC
CTTATGACCTCTACCATCCCTTCTCTCGGTGGGAGGCCACCCCATGGACCGGTGCTCCTCC
TCGTGTGGGGGGGCATCCAGAGCCGGGCAGTTTCTGTGTGGAGGAGACATCCAGGGGCA
TGTCACTTCAGTGGAAGAGTGGAAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCT
GCAACATTTTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGT
GGCCAGGCCTCAGATACCGTGTGGTCTCTGCACTCGACCATCGAGGAATGCACACAGGAGG
CTGTAGCCCAAAAACAAAGCCCCACATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATA
AACCCAAAGAGAAACTTCCAGTCGAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTA
GAAGAAGGAGCTGCTGTGTCAGAGGAGCCCTCGTAAAGTTGTAAAAGCACAGACTGTTCTATA
TTTGAAACTGTTTTGTTTAAAGAAAGCAGTGTCTCACTGGTTGTAGCTTTTCATGGGTTCTGA
ACTAAGTGTAATCATCTCACCAAGCTTTTTGGCTCTCAAATTAAGATTGATTAGTTTCAA
AAAAAAAA

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FIGURE 120

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847

<subunit 1 of 1, 525 aa, 1 stop

<MW: 58416, pI: 6.62, NX(S/T): 1

MECCRATPGTLLLLFLAFLLLSSRTARSEEDRDGLWDAGFPWSECSRTC GGGASYSLRRLCS
SKSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNDPDNPSLKCQ
AKGTTLVVELAPKVLGDGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCR
LVRGQYKSQLSATKSDDTVVALPYGSRHIRLVLKGPDLHLYLETKTLQGTGENSLSSSTGTFL
VDNSSVDFQKFPDKEILRMAGPLTADFI VKIRNSGSADSTVQFIFYQPIIHRWRETDFFPSCS
ATCGGGYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDPCPASDGYKQIMPYD
LYHPLPRWEATPWTACSSSCGGGIQSRVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNI
FDCPKWLAQEWSPTVTGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPK
EKLPVEAKLPWFKQAQELEEAAVSEEPS

Important features:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 251-254

Thrombospondin 1

amino acids 385-399

von Willebrand factor type C domain proteins

amino acids 385-399, 445-459 and 42-56

0078561-101601

FIGURE 121

CGGACGCGTGGGCGGCGGCTGCGGAACTCCCGTGGAGGGGCCGTTGGGCCCTCGGGCCTGAC
AGATGGCAGTGGCCACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGGCGCTGTGGCTGGCG
GCCCCGCGGTTTCGTGGGGCCAGGGTCCAGCGGCTGCGCAGAGGCGGGGACCCCGGCTCAT
GCACGGGAAGACTGTGTGATCACCAGGGGCGAACAGCGGCTGGGCCGCGCCACGGCCGCGG
AGCTACTGCGCCTGGGAGCGCGGGTGATCATGGGCTGCCGGGACGCGCGCGCGCCGAGGAG
GCGGCGGGTCAGTCTCCGCGCGAGCTCCGCCAGGCCGCGGAGTGCGGCCACAGACCTGGCGT
CAGCGGGGTGGGCGAGTCTATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCG
CCTTCTGCCAGGAAATGCTCCAGGAAGAGCCTAGGCTGGATGTCTTGATCAATAACGCAGGG
ATCTTCCAGTGCCCTTACATGAAGACTGAAGATGGGTTTGAGATGCAGTTCGGAGTGAACCA
TCTGGGCACTTTCTACTACCAATCTTCTCCTGGACTCCTCAAAAGTTCAGTCCCAGCA
GGATTGTGTAGTCTTCTCCAACTTTATAAATACGGAGACATCAATTTTGATGACTGAAC
AGTGAACAAAGCTATAATAAAAGCTTTGTATAGCCGAGCAAACCTGGCTAACATTCCTTTT
TACCAGGGAAGTACCCCGCGCTTAGAAGGCACAAATGTACCGTCAATGTGTGTCATCCTG
GTATTGTACGGACAAATCTGGGGAGGCACATACACATTCCACTGTGTGGTCAAACCACTCTTC
AATTGGTGTGTCATGGGCTTTTTTCAAACCTCCAGTAGAAGGTGCCAGACTTCCATTTATTT
GGCCTCTTACCTGAGGTAGAAGGAGTGTGAGGAAGATACCTTGGGGATTGTAAAGAGGAAG
AACTGTTGCCCAAAGCTATGGATGAATCTGTTGCAAGAAAACCTCGGGATATCAGTGAAGTG
ATGGTTGGCCTGCTAAATAGGAACAAGGAGTAAAGAGCTGTTTATAAACTGCATATCAG
TTATATCTGTGATCAGGAATGGTGTGGATTGAGAAGTGTACTTGAAGAAAAAGAAATTTG
ATATTGGAATAGCCTGCTAAGAGGTACATGTGGGTATTTTGGAGTTACTGAAAAATATATTT
TGGGATAAGAGAAATTCAGCAAAGATGTTTTAAATATATATAGTAAGTATAATGAATAATAA
GTACAATGAAAAATACAATTATATTGTAAATTTATACTGGGCAAGCATGGATGACATATTA
ATATTTGTGAGAATTAAAGTACTCAAAGTGCTATCGAGAGTTTTTCAAGTATCTTTGAGTT
TCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTTTGTGTGGAAATTTATCTGC
CTGGTGTGTGCACACAAGTCTTACTTGAATAAAATTTACTGGTAC

09978564-101601

Figure 1. The effect of the concentration of the *Agrobacterium* suspension on the transformation efficiency of *Agrobacterium* strains. The concentration of the *Agrobacterium* suspension was 10⁶ cells/ml (a), 10⁷ cells/ml (b), 10⁸ cells/ml (c), and 10⁹ cells/ml (d). The concentration of the *Agrobacterium* suspension was 10⁶ cells/ml (a), 10⁷ cells/ml (b), 10⁸ cells/ml (c), and 10⁹ cells/ml (d).

<subunit 1 of 1, 336 aa, 1 stop

MAVATAAAVLALGGALWLAARRFVGPRVQRLRGGDGPLMHGKTVLITGANSGLGRATAAE
LLRLGARVIMGCFDRARAEEBAAGQLRRELRLQAECGPEPGVSGVGELIVRELDLASLRSVRA
FCQEMLQEEPRLDVLINNAGIFQCPLYMKTEDGFEMQFVGNHLGHFLLTNLLLGLLKSSAPSR
IVVVSSKLYKYGDINFDDLNSEQSYNKSFCYSRSLKANILFTRELARRLEGNTVNTVNLVHPG
IVRTNLGRHIHPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPESVGRYFGDCKEE
LLPKAMDESVARGLKLSIEMVGLLK

Signal peptide:

Short-chain alcohol dehydrogenase family protein

amino acids 134-144, 44-56 and 239-248

N-glycosylation site.

amino acids 212-215 and 239-242

FIGURE 123

GGGGATTGTAAAGAGGAAGNACTGTGCCCAAAGNTATGGATGAATCTGTTGCAAGAAAATTN
TGGGATATCAGTGAAGTGATGGTTNGCCTGCTAAATAGGAACAAGGAGTAAAAGAGCTGTT
TATAAACTGCATATCAGTTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACT
TGAAGAAAAAGAAATTTTGATATTGGAATAGCCTGNTAAGAGGNACATGTGGGTATTTTGGAG
T TACTGAAAAATTATTTTGGGATAAGAGAATTT CAGCAAAGATGTTTTAAATATATATAGT
AAGTATAATGAATAATAAGTACAATGAAAAATACAATTATATTGTAAAAATTATAACTGGGCA
AGCATGGATGACATATTAATATTTGT CAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTT
TTCAAGTATCTTTGAGTTTCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTT
TGTGTGGAATTATCTGCCTGGCTT

0997854.101501

FIGURE 124

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCCGCTCCCGAGCCCAGCC
CTTTCCCTAACCCAAACCCAACTAGCCAGTCCAGCCGCCAGCGCTGTCCCTGTACGGAC
CCCAGCGTTACATGCATCCTGCCGTCCTCTATCCTTACCCGACCTCAGATGCTCCCTTCT
GCTCCTGGTAACTTGGGTTTCTTACTCCTGTAACTGAAATAACAAGTCTTGCTACAGAGA
ATATAGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTATGCTGACTGGTGT
CGTTTCAGTCAGATGTTGCATCCAATTTTGGAGGAAGCTTCCGATGTCATTAAGGAAGAATT
TCCAAATGAAATCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCC
AGAGATACAGGATAAGCAAATACCCAACTTCAAATGTTTCGTAATGGGATGATGATGAAG
AGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTTGGCAGATTACATCAGGCAACAAAAAG
TGACCCCATTCAGAAATTCGGGACTTAGCAGAAATCACCCTCTTGATCGCAGCAAAAGAA
ATATCATTTGGATATTTTGAGCAAAAGGACTCGGACAATATAGAGTTTTTGAACGAGTAGCG
AATATTTTGCATGATGACTGTGCCCTTCTTTCTGCATTTGGGGATGTTTCAAACCGGAAAG
ATATAGTGGCGACAACATAATCTACAAACCACAGGGCATTCTGCTCCGGATATGGTGTACT
TGGGAGCTATGACAAATTTTGATGTGACTTACAATTTGGATTCAAGATAAATGTGTTCTCTTT
GTCCGAGAAATAACATTTGAAATGGAGAGGAATTGACAGAAGAAGGACTGCGCTTTTCTCAT
ACTCTTTCACATGAAAGAAGATACAGAAAGTTTAGAAATATTCAGAATGAAGTAGCTCGGC
AATTAATAAGTGAAAAAGGTACAATAAACTTTTTACATGCCGATTGTGACAAATTTAGACAT
CCTCTTCTGCACATACAGAAAACCTCCAGCAGATTGCTCTGTAATCGCTATTGACAGCTTTAG
GCATATGTATGTGTTTGGAGACTTCAAAGATGTATTAATTCCTGGAAAACCAAGCAATTG
TATTTGACTTACATTCTGGAAAACCTGCACAGAGAATTCATCATGGACCTGACCCAACTGAT
ACAGCCCCAGGAGAGCAAGCCCCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAA
ACTAGCACCCAGTGAATATAGGTATACTCTATTGAGGGATCGAGATGAGCTTTAA~~AAAA~~AACTTG
AAAAACAGTTTGTAAAGCCTTTCACAGCAGCATCAACCTACGTGGTGGAATAGTAAACCTA
TATTTTCATAATCTATGTGTATTTTATTTTGAATAAACAGAAAGAAATTTAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 125

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57689
<subunit 1 of 1, 406 aa, 1 stop
<MW: 46927, pI: 5.21, NX(S/T): 0
MHPAVFLSLPDLRCSLLLLVTWVFTPVTTEITSLATENIDEILNNADVALVNFYADWCRFSQ
MLHPIFEEASDVKEEFFNENQVVFARVDCDQHS DIAQRYRISKYPTLKLFRNGMMMKREYR
GQRSVKALADYIRQQKSDPIQEIRDLAEITTLDRSKRNIIGYFEQKSDSNYRVFVERVANILH
DDCAFLSAFGDVS KPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDVTYNWIQDKCVPLVREI
TFENGEELTEEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLH
IQKTPADCFVIAIDSFRHMYVFGDFKDVLI PGKLKQFVFDLHSGKLHREFHHGPDPTDTAPG
EQAQDVASSPPESSFQKLAPSEYRYTLLRDRDEL

Important features:

Signal peptide:

amino acids 1-29

Endoplasmic reticulum targeting sequence.

amino acids 403-406

Tyrosine kinase phosphorylation site.

amino acids 203-211

Thioredoxin family proteins

amino acids 50-66

0978554 101601

FIGURE 126

ATTAAGGAAGAATTTCCAAATGAAAATCAAGTAGTNTTTGCCAGAGTNGATTGTGATCAGCA
CTCTGACATAGCCCAGAGATACAGGATAAGCAAATACCCAACCCCTCAAATTGTTTCGTAATG
GGATGATGATGAAGAGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTA

109101-109101

FIGURE 127

AGAGGCCTCTCTGGAAGTTGTCCCGGGTGTTCGCCGCGAGAGCCCGGTCGAGAGGACNAGG
TGCCCGCTGCCTGGAGAATCCTCCGCTGCCGTCGGCTCCCGAGCCCAGCCCTTTCCTAACCC
AAGCCAACTAGCCCNCTCCAGCCGCCAGCGCTGTCCCTGTCTCNGGANCCAGCGTNACC
ATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCTCCTGGTAAC
TTGGGTTTTTACTCCTGTAACAACCTGAAATAACNNGTCTTGATACNNAGAAATATAGATGAAA
TTTTAAACNATGCTGATGTGGCTTTAGTCAATTTTTATGCTGACTGGTGTCTCGTTTCAGTCAG
ATGTGGCATCCAATTTTTGAGGANGCTTCGATGTCATTAAGGAAGAATTTCCAAATGAAAA
TCAAGTAGTGTGTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATACAGGA
TAAGCAAATACCCAACCTCAAATTGTTTCGTAATGGGATGATGATGAAGAGAGAATACAGG
GGTCAGCGATCAGTGAAAGCATTTGGCAGATTACATCAGGC

FIGURE 128

GCCACGCGTCCGATGCGGTTACGTTTCGCGGCCTTCTGCTACATGCTGGCGCTGCTGCTCA
CTGCGCGCTCATCTTCTTCGCCATTGCGACATTATAGCATTGATGAGCTGAAGACTGAT
TACAAGAATCCTATAGACCAGTGTAATACCCCTGAATCCCCCTTGTA^{CT}CTCCAGAGTACCTCAT
CCACGCTTCTTCTGTGTCTGTTCTTGTGTCAGCAGAGTGGCTTACACTGGGTCTCAATA
TGCCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCAGGA
CTCTATGACCCACAACCATCATGAATGCAGATATTTCTAGCATATTGTGAGAAGGAAGGATG
GTGCAAAATTAGCTTTTTATCTTCTAGCATTTTTTACTACCTATATGGCATGATCTATGTTT
TGGTGAGCTCTTTAGAACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCAC
CAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGT
TACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTGTCTGTGGAAAGACTG
TTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAAATTAATATAAAAT
GATTACCTCTGGTGTTGACAGGTTTGAACCTGCACCTCTTAAGGAACAGCCATAATCCTCTG
AATGATGCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTGTTTATAGGAACCTGTA
GGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAAATTAGCTGTAGATATCAGGTGC
TTCTGATGAAGTGAAATGTATATCTGACTAGTGGGAACTTCATGGGTTTCTCATCTGTC
ATGTCGATGATTATATATGGATACATTTACAAAAATAAAAGCGGGAATTTTCCCTTCGCTT
GAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAA
TATACTTGCTTTAATTCTTAAGCATAAGTAAACATGATATAAAAAATATATGCTGAATTACTT
GTGAAGAAATGCATTTAAAGCTATTTTAAATGTGTTTTTATTTGTAAGACATTACTTATTAAG
AAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTGTCAGG
TACTACAGATTTTCAAACCTGAATGAGAGAAAATTGTATAACCATCCTGCTGTTCTTTAGT
GCAATACAATAAACTCTGAAATTAAGACTC

09/8564.10607

FIGURE 129

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330
<subunit 1 of 1, 144 aa, 1 stop
<MW: 16699, pI: 5.60, NX(S/T): 0
MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFF
CVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPLYDPTTIMNADILAYCQKEGWCKLA
FYLLAFFYYLYGMIYVLVSS

Important features:

Signal peptide:

amino acids 1-20

Type II transmembrane domain:

amino acids 11-31

Other transmembrane domain:

amino acids 57-77 and 123-143

00978664-101001

FIGURE 130

ATTATAGCATTTGATGAGCTGAAGACTGATTACAAGATCCTATAGACCAGTGTAAATACCTG
AATCCCCCTGTACTCCCAGAGTACCTCATCCACGCTTTCCTTGTGTGCATGTTTCTTTGTGC
AGCAGAGTGGCTTACACTGGGTCTCAATATGCCCCCTCTTGGCATATCATATTTGGAGGTATA
TGAGTAGACCAGTGATGAGTGGCCCAGGACTCTATGACCCTACAACCATCATGAATGCAGAT
ATTCTAGCATATTGTCAGAAGGAAGGATGGTGCAAATTAGCTTTTTATCTTCTAGCATTTT
TTACTACCTATATGGCATGATCTATGTTTTGGTGAGCTCTTAGAACACACACAGAAGAATT
GGTCCAGTTAAGTGCAATGCAAAAAGCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGT
CCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAAAAAATG

09978564-101601

FIGURE 131

CGGACGCGTGGGGGAAACCCCTCCGAGAAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGG
GAACAAGATGCGCGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAACCTGGGGCTCCCGCCG
TGTGCTGCTGACCATGGCCTTGGCCGGAGGTTGCGGGACCGCTTCGGCTGAAGCATTGTGAC
TCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGCACAC
CTACCCTAAGGAAGAGAGATTGTACGCATGTCAGAGAGTTGCAGGCTGTTTTCAATTTGTC
AGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTTGGAATGTGAATCTGCATGTACA
GAAGCATATTTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCC
ATTCGCTGAAC TGAGACAAGAACAACTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTC
CTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACC
TCTTCATGGACTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTATATTCAGTCTAAGCC
AGAAATCCAGTACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAA
GCAAAATGTCTTATCTGCAAATGAGAAATTCACAAGCGCACAGGAATTTTCTTGAAGATGGA
GAAAGTGATGGCTTTTAAAGATGCCTCTCTCTTAACTCTGGGTGGATTTTAACTACAACTCT
TGTCTCTCGGTGATGGTATTGCTTTGGATTGTTGTGCAACTGTTGCTACAGCTGTGGAGC
AGTATGTTCCCTCTGAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAG
CTAAACAGATATCCAGCTTCTTCTCTTGTGGTTGTTAGATCTAAAAC TGAAGATCATGAAGA
AGCAGGGCCTCTACCTACAAAAGTGAATCTTGCTCATTCTGAAATTTAAGCATTTTTCTTTT
AAAAGACAAGTGTAATAGACATCTAAAATTCACCTCCTCATAGAGCTTTTAAAAATGGTTTCA
TTGGATATAGGCCTTAAGAAATCACTATAAAATGCAAATAAAGTTACTCAAATCTGTG

007554.10160

FIGURE 132

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26847
<subunit 1 of 1, 323 aa, 1 stop
<MW: 36223, pI: 5.06, NX(S/T): 1
MAAPKGS LWVRTQLGLPPLLLLTMALAGGSGTASAEAFDSVLGDTASCHRA CQLTYPLHTYP
KEEELYACQRCRLFSICQFVDDGIDLNR TKLECESACTEAYSQSDEQYACHLGCQNQLPFA
ELRQEQQLMSLMPKMHLLFPLTLVRSFWS DMMSAQSFITSSWTFY LQADDGKIVIFQSKPEI
QYAPHLEQEPTNLRESSLSKMSYLQMRNSQAHRNFLEDGESDGFRLCLSLNSGWILTTTLVL
SVMVLLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVRSKTEDHEEAG
PLPTKVNLAHSEI

Important features:

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 241-260

N-glycosylation site.

amino acids 90-93

FIGURE 133

TTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGACACCTACCC
TAAGGAAGAGGAGTTGTACGCATGTACAGAGAGGTTGCAGGCTGTTTTCAATTTGTAGTTTG
TGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA
TATTCCTCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCCATTGCG
TGAACGAGACAAGAACAACCTTATGTCCCTGATGCCAAAATGCACCTACTCTTTCCTCTAA
CTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGC

097854.101601

FIGURE 134

CACACTGGCCGGATCTTTTAGAGTCCTTTGACCTTGACCAAGGGTCNGGAAAAACAGCAACAA
GCTGAGCTGCTGTGACAGAGGGAACAAGATGGCGGCGCCGAAGGGAGCCTTTGGGTGAGGAC
CCAAC TGGGGCTCCGCGCTGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTCTGGGGACCG
CTTCGGCTGAAGCATTTGACTCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCTAG
TTGACCTACCCCTTGACACCTACCCTAAGGAAGAGGAGTTGTACGCATGTCTAGAGAGGTTG
CAGGCTGTTTCAATTTGTCTAGTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGG
AATGTGAATCTGCATGTACAGAAGCATATTCCTAATCTGATGAGCAATATGCTTGCCATCTT
GGTTGCCAGAATCAGCTGCCATTGCTGAACTGAGACAAGAACAACCTTATGTCCTGATGCC
AAAAATGCACCTACTCTTCCTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACT
CCGC

0978554-101001

FIGURE 135

GCGAGGTGGCGATCGCTGAGAGGCAGGAGGGCCGAGGCGGGCCTGGGAGGCGGCCCGGAGGT
GGGGCGCGCTGGGGCCGGCCCGCACGGGCTTCATCTGAGGGCGCACGGCCCGCGACCGAGC
GTGCGGACTGGCCCTCCCAAGCGTGGGGCGACAAGCTGCCGAGCTGCAATGGGCCGCGGCTG
GGGATTCTTTGTTTGGCCTCCTGGGCGCGTGTGGCTGCTCAGCTCGGGCCACGGAGAGGAGC
AGCCCCCGAGACAGCGGCACAGAGGTGCTTCTGCCAGGTTAGTGGTTACTTGGATGATTGT
ACCTGTGATGTTGAAACCATTGATAGATTTAATAACTACAGGCTTTTCCCAAGACTACAAAA
ACTTCTTGAAAGTGACTACTTTAGGTATTACAAGGTAAACCTGAAGAGGCCGTGTCTTTCT
GGAATGACATCAGCAGTGTGGAAGAAGGGACTGTGCTGTCAAACCATGTCAATCTGATGAA
GTTCTGATGGAATTAATCTGCGAGCTACAAGTATTCTGAAGAAGCCAATAATCTCATTGA
AGAATGTGAACAAGCTGAACGACTTGGAGCAGTGGATGAATCTCTGAGTGAGGAAACACAGA
AGGCTGTTCTTCAGTGGACCAAGCATGATGATTCTTCAGATAACTCTGTGAAGCTGATGAC
ATTGAGTCCCTGAAGCTGAATATGTAGATTGCTTCTTAATCCTGAGCGCTACACTGGTTA
CAAGGGACCGAGTGTCTGGAATAATGGAATGTCTACGAAGAAAACTGTTTAAAGCCAC
AGACAATTAAAGACCTTTAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGAACACT
TTTTACAGTTGGCTAGAAGGTCTCTGTGTAGAAAAAGAGCATTTACAGACTTATATCTGG
CCTACATGCAAGCATTAAATGTGCATTTGAGTGAAGATATCTTTTACAAGAGACCTGGTTAG
AAAAGAAATGGGGACACAACATTACAGAATTTCAACAGCGATTGTATGGAATTTTGACTGAA
GGAGAAGGTCCAAGAAGGCTTAAGAACTTGATTTTCTCTACTTAATGAACCTAAGGGCTTT
ATCCAAAGTGTTACCAATCTTCGAGCGCCAGATTTTCAACTCTTTACTGGAAATAAAATTC
AGGATGAGGAAAACAAATGTACTTCTGGAATACTTTCATGAAATCAAGTCAATTCCTTTG
CATTTTGATGAGAATTCATTTTTGCTGGGGATAAAAAAGAAGCACACAACTAAAGAGGA
CTTTCGACTGCATTTTAGAAATATTCAAGAATTATGGATTGTGTTGGTTGTTTTAAATGTC
GTCTGTGGGGAAAGCTTCAGACTCAGGGTTTGGGCACTGCTCTGAAGATCTTATTTTCTGAG
AAATTGATAGCAAATATGCCAGAAAGTGGACCTAGTTATGAATTCATCTAACAGACAAGA
AATAGTATCATTATTCACGCAATTTGGAAGAATTTCTACAAGTGTGAAAGAATTAGAAAACT
TCAGGAACCTGTTACAGAATATTCATTAAAGAAAAACAAGCTGATATGTGCCTGTTTCTGGAC
AATGGAGGCCAAAGAGTGGAAATTTCAATCAAAGGCATAATAGCAATGACAGTCTTAAGCCAA
ACATTTTATATAAAGTTGCTTTTGTAAAGGAGAAATATATGTTTTAAGTAAACACATTTTT
AAAAATTGTGTTAAGTCTATGTATAATACTACTGTGAGTAAAAGTAATACTTTAATAATGTG
GTACAAATTTTAAAGTTAATATTGAATAAAAGGAGGATTATCAAATTAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

1397854.101601

FIGURE 136

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53974
<subunit 1 of 1, 468 aa, 1 stop
<MW: 54393, pI: 5.63, NX(S/T): 2
MGRGWGFLFGLLGAVWLLSSGHGEEQPPETAARCFQVSGYLDCTCDVETIDRFNNYRLF
PRLQKLLSDYFRYYKVNLRPCPFWNDSQCGRRDCAVKPCQSDDEVPDGIKSASYKYSEEA
NNLIEECQAEERLGAVDESLSEETQKAVLQWTKHDDSSDNFCEADDIQSPEABYVDLLLNP
RYTYGKGPDAWKIWNVIYEENCFKPQTIKRPLNPLASGQGTSEENTFYSWLEGLCVEKRAF
RLISGLHASINVHLSARYLLQETWLEKKWGHNITEFQQRFDGILTEGEGPRRLKNLYFLYLI
ELRALS KVLPPFFERPDFQLFTGNKIQDEENKMLLLEILHEIKSFPLHFDENSFFAGDKKEAH
KLKEDFRLHFRNISRIMDCVGCFCRLWGKLQTQGLGTALKILFSEKLIANMPESGPSYEFH
LTRQEIVSLFNAFGRISTSVKELENFRNLLQNIH

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 280-283 and 384-387

Amidation site.

amino acids 94-97

Glycosaminoglycan attachment site.

amino acids 20-23 and 223-226

Aminotransferases class-V pyridoxal-phosphate

amino acids 216-222

Interleukin-7 proteins

amino acids 338-343

1367554-11111

FIGURE 137

GCTGAAATATGGATGTCATCTACGAGAACTGTTTTAAGCCACAGACAATTTAAAGACCTT
TAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGNACACTTTTTACAGTTGGCTAGAA
GGTCTCTGTGTAGAAAAAGAGCATTCTACAGACTTATATCTGGCCTACATGCAAGCATTAA
TGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAGAAAAGAAATGGGGACACA
ACATTACAGAATTTNAACAGCGATTGTGATGGAATTTTGACTGAAGGAGAAGGTCCAAGAAGG
CTTAAGAAGTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTTATCCAAAGTGTACCATT
CTTNGAGCGCCAGATTTTCAACTNNTTACTGGAATAAAATTCAGGATGAGGNAAACAAAA
TGTTACTTTTGAAATACTTCATGAAATCAAGTCATTTCCTTTGCATTTTGATGAGAATTCA
TTTTTTTGCTG

0997664-101601

FIGURE 138

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTTGGGAGGGGGCAGGATGGGAGGGAA
AGTGAAGAAAAAGAGAGGGGACAGAGGCCAGAGGACTTCTCATACTGGACAGAAAC
CGATCAGGCATGGAACTCCCCCTTCGTCACTCACCTGTTCTTGCCCTGGTGTTCTTGACAGG
TCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCTATTCCAGGGCCACCAGAAG
CTGAATTTGGATACAGTGTCTTACACATGTTGGGGGTGGACAGCGATGGATGCTGGTGGGC
GCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTTTATCGCTGCCCTGTAGGGGG
GGCCCAATGCCCATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGGAAATTCTCTC
ATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGACAGATGGTGATGGGGGATTC
ATGGTGAGCTAAGGAGAGGGTGGTGGCAGTGTCTCTGAAGGTCCATAAAAGAAAAAGAGAA
GTGTGGTAAGGAAAAATGGTCTGTGTGGAGGGGTCAAGGAGTTAAAAACCTAGAAAGCAAA
AGGTAGGTAATGTGAGGGAGTAGTCTTCATGCCTCCTTCAACTGGGAGCATGTTCTGAGGGT
GCCCTCCCAAGCCTGGGAGTAACATATTCCCCCATCCCCAGGCCCTGTGCCCTCTCTGGTCT
CGTGCTTGTGGCAGCTCTGTCTTCAGTTCTGGGATATGTGCCCGTGTGGATGCTTCATTCCA
GCCTCAGGGAAGCCTGGCACCCACTGCCCAACGTGAGCCAGAGGAAGGCTGAGTACTTGGTT
CCCAGAAGGAGATACTGGGTGGGAAAAAGATGGGGCAAAGCGGTATGATGCCCTGGCAAAGGG
CCTGCATGGCTATCCTCATTGCTACCTAATGTGCTTGCAAAAGCTCCATGTTTCTTAACAGA
TTCAGACTCCTGGCCAGGTGTGGTGGCCACACCTGTAATTCTAGCACTTTGGGAGGCCAAG
GTGGGCAGATCACTTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACTCCAT
CTCTACTAAAAAATAACAAAAATTAGCTGGGTGCGCTAGTGATGCCCTGTAATCTC
ATCTACTCGGGAGGCTAAGACAGGAGACTCTCACTTCAACCCAGGAGGTGGAGGTTGCGGTG
AGCCAAGATTGTGCCCTCTGCACTCTAGCGTGGGTGACAGAGTAAGCGAGACTCCATCTCAA
AATAATAATAATAATTCAGACTCCTTATCAGGAGTCCATGATCTGGCCTGGCACAGTAA
CTCATGCCCTGTAATCCCAACATTTTGGGAGGCCAACGCAGGAGGATTGCTTGAGGTCTGGAG
GTTTGAGACCAGCCTGGGCAACATAGAAAGACCCCATCTCTAAATAAATGTTTTAAAAAT

03754.11601

2025年1月1日

```
><subunit 1 of 1, 124 aa, 1 stop
```

MELPFVTHLFLPLVFLTGLCS PFNLDEHHPRLFP GPPEAEFGYSVLQHVG GGGQRWMLVGAPW

DGPSGDRRGDVYRCPVGGAHNAPCAKGHLGDYQLGNSSHPAVNMHLGMSLLETGDGGGFMS

Signal peptide:

Cell attachment sequence.

N-glycosylation site.

amino acids 98-101

Integrins alpha chain proteins

amino acids 67-81

FIGURE 140

CACAGTTCCTCCACCATCACTCNTCCCATTCCTTCCAACCTTATTTTTAGCTTGCCATTGGGA
GGGGGCAGGATGGGAGGGAAAAGTGAAGAAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGAC
TTCTCATACTGGACAGAAACCGATCAGGCATGGAACCTCCCCTTCGTCACTCACCTGTTCTTG
CCCCTGGTGTTCCTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCT
ATTCCCAGGGCCACCAGAAGCTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGAC
AGCGATGGATGCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGAGGGGGGACGTT
TATCGCTGCCCTGTAGGGGGGGCCCAATGCCCATGTGCCAAGGGCCACTTAGGTGACTA
CCAAC TGGGAAATTCATCTCATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGA
CAGATGGTGATGG

0097554.10601

FIGURE 141

AAGTTACATTTTCTCTGGAACTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
 GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCTGGGCCGGCTCTAGAACA
 ATTCAAGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
 GAGATGGACAGAATGCTTTATTCTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA
 AATGCAGACTTTCACAAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
 ACGCATTGATTCCATGTTTGGCTCACAGATGAAGTGCCATTCTGCCTGCCCTCAGAACCTC
 TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCCTGGAGA
 AACAGTGTACTATTCTGTGCAATACCAGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
 GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGTCTGAGTGTGATGTCACTGATGACATC
 ACGGCCACTGTGCCATACAACCTTCGTGTGAGGGCCACATTGGGCTCACAGACCTCAGCCTG
 GAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTACCCGACCTGGGATGGAGA
 TCACCAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCAAGTTTGAGTTC
 CTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG
 GGGTATTCCAGTGCCACTAGAAACCATGGAGCCAGGGCTGCATACTGTGTGAAGGCCGAGA
 CATTCGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
 GGAGAGGCCATTCCCTGGTACTGGCCCTGTTTGCCTTTGTTGGCTTCATGCTGATCCTTGT
 GGTCTGTCCTGTTCTGTCTGAAAAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCGCTGG
 TGGTCTCCAGACACCTTGAAATTAACCAATTACCCAGAAAGTTAATCAGTCTGCAGAAAG
 GAGGAGGTGATGCTCTGTGCCACGGCTGTGATGTCTCTGAGGAACTCCTCAGGGCCTGGAT
 CTCATAGGTTTGGGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAACC
 ATGAGGGGACAAGTTGTGTTTCTGTTTTCGCCACCGGACAAGGGATGAGAGAAGTAGGAAGA
 GCCTGTTGTCTAAGTCTAGAAGCAACCATCAGAGGCAGGGTGTTTGTCTAACAGAAACAC
 TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGGCTGCCACTTGTCTGGCTGAGCAACC
 CTGGGAAAGTGACTTTCATCCCTTCGGTCTTAAGTTTCTCATCTGTAAATGGGGGAATTACC
 TACACACCTGCTAAACACACACACAGAGTCTCTCTATATATACACAGTACACATAAA
 TACACCCAGCACTTGCAAGGCTAGAGGGAACTGGTGACACTCTACAGTCTGACTGATTAG
 TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
 GGCTTGGAGAGCCCACTTTCAGAAATAATCCTTGAGAGAAAGGAATCATGGGAGCAATGG
 TGTTGAGTTCACTTCAAGCCCAATGCCGCTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGT
 AGGTGACCTGGAGGAAGGTACAGCCACACTGAAAAATGGGATGTGCATGAACACGGAGGATC
 CATGAACACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
 GTGCAATGCAGCAGAAATGCAGAAAGTCACTAATGTGCATGTTTGTGTGCTCCTTTTTC
 GTTGGTAAAGTACAGAATTCAGCAAATAAAAGGGCCACCTTGCCAAAAGCGGTAAAAAA
 AAAAAAAAAA

09978554 101601

FIGURE 142

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57033

<subunit 1 of 1, 311 aa, 1 stop

<MW: 35076, pI: 5.04, NX(S/T): 2

MQTFTMVLEEIWTSILFMWFFYALIFCLLTDEVAILPAPQNLSVLSTNMKHLMLWSPVIAPGE
TVVYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECVTDITATVPYNLRVRATLGSQTS
SILKHPFNRRNSTILTRPGMEITKDGPHLVIELEDLGPQFEFLVAYWRREPAAEEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECEVQGEAIPVLALFAFVGFMILILV
VVPLFVWKMGRLQLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation site.

amino acids 40-43 and 134-137

Tissue factor proteins.

amino acids 92-119

Integrins alpha chain proteins

amino acids 232-262

007366-104601

FIGURE 143

TCCTGCTGATGCACATCTGGGTTTGGCAAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATT CAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCTGGAGAAAACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGTCCTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTCAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCTTGTTGGCCTANTGGAGGAGGGGCGAACCCTTGCGGCGCAAGGG
GTTNGGAAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCC
ACATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

0997854-10461

THE **NEW** **YORK** **PUBLIC** **LIBRARY**

CCACGCGTCCGCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAAACAGGGAGAAGA
GGCAGGAGAGGAGGAGGTGGGGAGAGCA CGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGA
GGAGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAGAGGAGAGAGGAGGAGGAG
GAGGAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAAC
GGAGAGGAGGTGTGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGA
GTAGGAAGATCAGGAGCTAGAGGGAGACTGGAGGTTCCGGGAAAAGAGCAGAGGAAGAGG
AAAGACACAGAGAGACGGGAGAGAGAAGAAGAGTGGGGTTGAAAGGCGGATCTCAGTCCCTG
GCTGCTTTGGCATTTGGGGAATGGGACTCCCTGTGGGGAGGAGAGGAAGAGCTGGAAGTCTCT
GGAGGGACAGGGTCCCAGAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGGCGAGGCGTTGGG
CAGGGGTCCCTCGGAGGCCCTCTGGGGAATGGGGGCTGCAGCTCGTCTGAGCGCCCTCGAGC
GCTGGTACTCTGGGCTGCAGTGGGGGCAGCAGCTCACATCGGACCAGCACCTGACCCCGAGG
ACTGTTGAGCTACAAGGATAATCTCCAGGGAACCTTCGTGCCAGGGCCTCCTTTCTGGGGC
CTGTTGAATGACGCGTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCCGTGATGTGGA
GCTGAAGAGGGTTCTTTATGACCCCTTTCTGCCCCCATTAAGGCTCAGCACTGGAGGAGAGA
AGCTCCGGGGAACCTTGTAACAACCGGCCGACATGTCTCCTTCCTGCTGCACCCCGACCT
GTGTTCAATGTGCTCGGAGGTCCCTCTCTTTACAGCACCCGACTCAGTGAACCTCGGGCTGTG
GTTTGGAGACTCGCAGCGAGGACCGGCTCGGTAACATCAGATCAACCAACCAAGGCTTCTCTGTG
AGGTGCAGCTCATTCACTTCAACCAGGAACCTCTACGGGAATTTACGCGCTGCCTCCGCGGC
CCCAATGGCCTGGCCATTCTCAGCCTCTTTGTCAACGTTGCACGTACCTCTAAACCCATTCT
CAGTCGCCTCCTTAACCGCGACACCATCACTCGCATCTCCTACAAGAATGATGCCTACTTTC
TTCAAGACCTGAGCCTGGAGCTCCTGTTCCCTGAATCCTTCGGCTTCATCACCTATCAGGGC
TCTCTCAGACCCCGCCTGCTCCGAGACTGTCACTGGATCTCATTGACCGGGCCCTCAA
TATCACTCCCTTCAGATGCAGCTCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCT
TCCAGAGCCTCAGCGGTAACAGCCGGCCCCCTGCAGCCCTTGGCCACAGGGCACTGAGGGGC
AACAGGACCCCGGCCACCCCGAGAGCGCTGCAGGCCCCAACCTACCGCTGCTGATGTGGA
TGGTGTCCCCATGCTCGCTGAGACTCCCTTCGAGGATTGACCCCGCTCTTAAGCCTC

FIGURE 145

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34353

<subunit 1 of 1, 328 aa, 1 stop

<MW: 36238, pI: 9.90, NX(S/T): 3

MGAAARLSAPRALVLWAAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLC
AVGKRQSPVDVELKRVLYDPFLPPLRLSTGGKLRGTLYNTGRHVSFLPAPRPVVNVSGGPL
LYSHRSELRLLLFGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSL
FVNVASTSNPFLSRLLLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITTYQGSLSLTPPCSE
TVTWILIDRALNITSLQMHSRLRLSQNPFSQIFQSLSGNSRPLQPLAHRALRGNRDPRHPER
RCRGPNYRLHVDGVPHGR

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 177-199

N-glycosylation site.

amino acids 118-121, 170-173 and 260-263

Eukaryotic-type carbonic anhydrases proteins

amino acids 222-270, 128-164 and 45-92

00075564-101601

FIGURE 146

GGCGCCTGGTTCTGCGCGTACTGGCTGTACGGAGCAGGAGCAAGAGGTGCGCGCCAGCCTCGCGCGCGAGCCTC
 GTTGTGTGTCGCCGCCCTCGCTGCTGCTGAGCTACTGCTCAGAAACGCTGGGGCGCCACCTGGCAGACTAACGAA
 CGCAGTCCCTTTCCCAACCCCACTGCAAGGTCTAATTTTGAGCGCTTTGGCCTGCCATTTCTTCAGAGTTGAGGGAGC
 GCGAGGCGGGAGGCTCGCGTATTCTGCACTCAGCAACCCACGCTCGCCCCCGGAGCGCTCGGTGCTCAGGCGCCTTC
 GCGAGCGGGGCTCTCCGTCTCGCGTCCCTTGTGAAGGCTCTGGCGGCTGCGAGGGCGGGCGCTCCGGTTTGGCT
 CACCTCTCCAGGAACTTCACTCGTGGAGAGCGAAAGGAGTGGAGAGGCTGTCTTGAGAGATTTTCTGGGGAA
 ATCCTGAGGTCATTCTATGAAAGTGTACCGCGCGGAGTGGCTCAGAGTAAACCAAGTGTCTGTTTCATGGCTAGA
 GCAATTTCCAGCCATGGTGGTTCCCAATGCCACTTTATTGGAGAACTTTTGGAAAAATACATGGATGAGGATGGT
 GAGTGGTGGATAGCCAAACCAACAGGGGAAAGGGCCATCAGACAATGACATCGCAGAGTATTTTGGACCTTCAT
 AATAAATTACGAGTTCAGGTGTATCCACAGCCTCTAATATGGAGTATATGACATGAGGATGTAGAGCTGGAAAGT
 TTCTCAGAATCTCGGGCTGAAAGTTGCTTTGTGGAAACATGGAACTCGCAAGCTTGCTTCCATCAATTGGACAGAAT
 TTGGAGCACACCTGGGGAGATATAGGCCCCCGACGTTTCATGTACAATCGTGGTATGATGAAGTGAAGAGCTTT
 AGCTACCCATATGAAATGCAACCCATATTGTCCATTAGGTGTTCTGGCCCTGTATGTACACATTATACA
 CAGGTGCTGTGGGCAACTAGTAAACAGAATCGGTTGTGCCATTAAATTTGTGTCATAACATGAACATCTGGGGCGAG
 ATATGGCCCAAGCTGTCTACCTGGTGTGCAATTACTCCCAAAGGGAACCTGGTGGGGCCATGCCCTTTACAAA
 CATGGGCGGCCCTGTTCTGCTTGCCCACTAGTTTGGAGGGGGCTGTAGAGAAAAATCTGTGCTACAAAGAGGG
 TCAGACAGGTATTATCCCCCTCGAGAAGAGGGAACAAATGAAATAGAACGACAGCAGTCACAAGTCCATGACACC
 CATGTCCGACACAGATCAGATGATAGTAGCAAAATGAAGTCATAAGCGCACAGCAAAATGTCCCAAATTTGTTCT
 TGTGAAGTAAGATTAAAGAGTCAAGTCAAGGGAACCAACTGCAATAGGTGACAGATGTCTGCTGGCTGTTTGGAT
 AGTAAAGCTAAAGTTATTGGCAGTGATCATTATGAAATGCAATCCAGCATCTGTAGAGCTGCAATTCATTATGGT
 ATAATAGACAATGATGGTGGCTGGGTAGATATCACTAGACAAGGAAGAACATTATTCATCAAGTCCAAATAGA
 AATGGTATTCAACCAATTTGGCAAAATCAGTCTGCTAATCCCTTCACAGTCTCTAAAGTCAAGCTCAGGCTGTG
 ACTTGTGAAACCAACTGTGGAAACAGCTCTGTCCATTTCATAAGCTGCTTCATCTGCCCAAGAGTATCTGTCTCT
 CGTAACTGTATGCAAGCAAAATCCACATTATGCTCGTGAATTTGGAACCTGAGTTTATCTGATCTGTGCAAGTATC
 TGCAGAGCAGCAGTACATGCTGGAGTGGTTCGAAATCAGCGTGGTTATGTTGATGTAAATGCTGTGACCAAGA
 AAGACCTACATGCTCTTTTTCAGAAATGGAATCTCTCAGAAAGTTTACAGAAATCTCCAGGAGGAAGGCAATTC
 AGAGTGTTTGTCTGTTGTGTAAGAACTGAATCTTGAAGAGGACCATAAAGACTATTCCAAATGCAATATTTCTGA
 ATTTTGTATAAACTGTAACTTACTGTACAGAGTACATCACTATTTTCAGCCCAAAAGGTCGCAAAATGCATA
 TAAATCTTGATAAACCAAGTCTATAAAATAAAACATGGGACATTAGCTTTGGGAAAAAGTAAATGAAAAATATATGG
 TTTTAGAAATCTCTGTGTTAAATATTGCTATATTTCTTAGCAGTTATTTCTACAGTTAATTACATGATCATGATT
 GTTCTACGTTTCTATATATATATGTTGCTTTGATATGCCACTAATAAAATGAATCTTAAACATTGAATGTGAATC
 GCCCTCAGCAATCATCTAGTGGCTTTAAAAATAATCGACTCTAAAACTGAAAGGAAACCTTATCACATTTTCCCC
 GTTCAATGCTTATGCCATTACCACTCCAAATAATCTCAATAATTTTCCACTTAATAACTGTAAAGTTTTTTTC
 TGTAAATTTAGGCAATAGAAATTAATTTCTGATATGCACTTCTATTTTATATAAAATAATCCTTTAAATATC
 CAAATGAATCTGTTAAATATGTTGATTCCTTGGGAATGGCCTTAAAAATAAATGATATAAAGTCAAGTGGTGGT
 ATGAAACATCTCTAGTGATCTGTAGTAAATGTAGGGTTAAGCATGGACGACGAGCTTTCTATGTACTGTTA
 AAATTGAGTGCATATTTCTTTTGTATCTCGCAAAATCTCCTGAGGCCAGGAAGTATAATAGCAAAAGTT
 GACAAAGATGAACATAATGTTATACATTACCATTGCACGTATTTTAAATGATAATGACCTTGTATATAA
 ATATTGCCATATCATGTACCTATAATGGTGATATATTGTTTCTATGAAAAATGTTATGTGCTTTGATACATAA
 AATCTGTAAAAATGTTAGTTTGGTAAATTTTTTCTGCTGTGGATTTACATATTAATTTTTCTGCTGGTGGGA
 TAACATTAATAATTAATCATGTTTCAAAAAAATAA

007-0000-10000

FIGURE 147

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417

<subunit 1 of 1, 500 aa, 1 stop

<MW: 56888, pI: 8.53, NX(S/T): 2

MKCTAREWLRVTTVLFMARAI PAMVVPNATLLEKLLLEKYMDEDGEWWIAKQRGKRAITDNDM
QSILDLHNKLR SQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPASLLPSIGQNLGAHW
GRYRPPTFHVQSWYDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQVWVWATSNRIGCAINLC
HNMNIWGQIWPKAVYLV CNYS PKGNWWGHAPYKHGRPC SACPPSFGGGCRENL CYKEGSDRY
YPPREETNEIERQQSQVHDTHVTRSDSSRNEVISAQQMSQIVSCEVRLRDQCKGTTTCNR
YEC PAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITRQGRKHYFIKSNRNGI
QTIGKYQSANSFTVSKVTVQAVTCE TTVEQLCPFHK PASHCPRVYCP RNCMQANPHYARVIG
TRVYSDLSSICRAAVHAGVVRNHGGYVDVMPVDK RKTYYIASFQNGIFSESLQNPPGGKAPRV
FAVV

Important features:

Signal peptide:

amino acids 1-20

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

N-glycosylation site

amino acids 28-31

109501-4258/560

FIGURE 148

GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGGCG
CAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCTGGGT
GGCGTCTCCGGGCCCGCTCCGACGGGCCAGCGCCCTCCCCATGCTCCCTGCTCCACGCCG
CGCCCTCCGGTCAGCATGAGGCTCCTGGCGCGCGCTGCTCCTGCTGCTGCTGGCGCTGT
ACACCGCGCTGTGGACGGGTCCAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTAC
AGCGACGTGAAGAAGCTGGAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGTTAT
CATCACCACCAAGAGCGTGTCCAGGTACCGAGGTGAGGAGCACTGCGCTGCACCCCAAGCTGC
AGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGGTCTACGAA
GAATAGGGTGAAAAAACCTCAGAAGGAAAACTCCAAACCAAGTTGGGAGACTTGTGCAAGGA
CTTTGCAGATTAAAAAAGGCTTTTC
TTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTACCAACGGTCAG
TTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCAGATGGGAGACCATCTCTCTTGTGCT
CCAGACTTCATCACAGGCTGCTTTTATCAAAAAGGGGAAAACTCATGSCCTTTCCTTTTAA
AAAATGCTTTTTTTGTATTGTGCCATACGTCACTATACATCTGAGCTTTATAAGCGCCCCGGA
GGAACAATGAGCTTGGTGGACACATTTCATTGCAAGTGTGCTCCATTCTAGCTTGGGAAGC
TTCCGCTTAGAGTCTCGGCCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCG
GTCACAGCCTCAGTGTGACTCCACAGTGGCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCT
CTGCATCTGTTCTCTGAGGAACCTCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCT
GGTTAATTTTTTACACACCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATC
CTTAAAGAAGGTGTGGGGTCTTCCCAACCTGAGGATTTCTGAAAGGTTTCAGAGTTCAATA
TTTAATGCTTCAGAAGCATGTGAGGTTCACCAACTGTGAGCAAAAAACCTTAGGAGAAAACT
TAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAA
AACCTTCAAGCATGTTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATAT
TTGTGATTTCCCATGTAAATCTTCAATGTTAAACAGTGCAGTCTCTTTTCGAAAGCTAAGAT
GACCATGCGCCCTTCTCTGTACATATACCTTAAGAACGCCCCCTCCACACTGCCCCC
CAGTATATGCGCATTGTACTGCTGTGTTATATGCTATGTACATGTGAGAAACCATTAGCAT
TGATGCAAGTTTCATATTCTTCTAAGATGGAAAGTAATAAATATATTGAAATGTAAAA
AAAAA

09478564.101601

FIGURE 149

MSLLPRRAPPVSMRLAAALLLLLLALY TARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPH
CEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNWNEKRRVYEE

Signal sequence:

amino acids 1-34

06978564.304601
109401-4958/660

FIGURE 150

GCCCAGGGACTGCTATGGCTTCCTTTGTTGTTACCCCGGTCTGCGTCATGTTAAATCCCAATGTCTCCTGTG
 GTTAACTGCTCTTGGCCATCAAGTTCACCCCTCATTGACAGCCAAAGCAGATATCCAGTTTGTCAACCAAAATTTATGG
 CAAAATCCGGGGCCCTAAGAACACCGTTACCCAAATGAGATCTTGGGTCCAGTGGAGCAGTACTTATGGGTCCCCATG
 TGCCTCACCCCCCACTGGAGAGAGGCGGTTTCAGCCCCCAGAACCCCGCTCTCTCGGACTGGCATCCGAAATAC
 TACTCAGTTTGTCTGCTGTGTGCCCCCAGCACTGGATGAGAGATCTTTATCATGACATGCTGCCATCTGCTTGT
 TACCGCCAAATTTGGTACTTTGATGACCTATGTTCAGATCAAAATGAAGACTGCCTTTACTTTAAACATCTACGT
 GCCACGGAGAGATGGAGCCCAACAAGAAAAACGCGAGATGATATAACGAGTAATGACCGTGGTGAAGACGAAGA
 TATTCATGATCAGAACAGTAAAGACCGCTCATGTCTATATCTCATGGGGGATCTTACATGAGAGGGCACCGGCAA
 CATGATTGACGGCAGCATTTTGGCAAGCTACGGAACCGTCATCGTATCACCATTAACCTACCGCTCGGGAATACT
 AGGGTTTAAAGTACCGGTGACACGGCAGCAAAAGGCAACTATGCGCTCTCGGATCAGATTCAAGCACTCGCGTG
 GATTGAGGAGAAATGGGAGCCCTTTGGCGGGGACCCCAAGAGAGTGACCATTTTGGCTCGGGGCTGGGGCCCTC
 CTGTGTCAGCCTGTTGACCTGTGCCACTACTCAGAGGCTCTTCCAGAAAGGCCATCATTCAGAGCGGGCACCGC
 CCTGTCCAGCTGGGCAGTGAATACACGCCCAGCAAGTACACTCGGATATTGGCAGACAAGGTGCGCTGCAACAT
 GCTGGACCAACGACATGGTGAATGCTGCGGGAACAAGAACTACAAGAGCTCATCCAGCAGACCATACACCC
 GGCCACCTACCATAGCCCTTCGGGCGGTTGATCGACGGGACGTCATCCAGACGCCCCCAAGATCTCTGATGGA
 GCAAGGCGAGTTCCTCAACTACGACATCATGTGCGGCGTCAACCAAGGGGAAGGCTGAAGTTCTGTGACGCGCAT
 CGTGGATAACGAGGACGGTGTGACGCCCAACGACTTTGACTTCTCGGTGTCAACTTCGTGGAACAACCTTTACCG
 CTACCTGAAGGGAAAGACACTTTTGGGGAGACTATCAAGTTTCATGTACACAGACTGGGCGGATAAGGAAAAACC
 GGAGACGCGGCGGAAACCCCTGGTGGCTCTCTTTACTGACCAACAGTGGGTGGCCCCCGCGGTGGCGCGGACCT
 GCACGCGAGTACGGCTCCCCACCTACTTCTATGCTTCTATCATCACTGCCAAAGCGAAATGAAGCCCGAGCTG
 GCGAGATTTCGGCCATGGTGTATGAGGTCCCTATGTCTTCGGCATCCCCATGATCGGTGCCACGAGCTCTTCAG
 TTGTAACCTTTCCAGAACCGAGCTCATGCTCAGCGCGGTGGTCATGACCTATGAGCAGAACTTCGCCAAAATCTGG
 TGATCCAAATCAACCGATTCTCAGGATACCAAGTTTCATTACACAAAACCCCAACGCTTTGAAGAAGTGGCTGG
 GTCCAAAGTATGATCCCAAGACGAGCTCTATCTGCAATTTGGCTTGAACCCAGAGATGAGAGATCACTACCGGGC
 AACCAAGGTGCTTCTGTGGAATCTGCTCTCATTTGCAACACTTGAAGCAGATTTCAAGTATGTTTCAAC
 AACCACCAAGCTTCTCCACAGACATGACATCATTTCCCTATGGCAACCGCGGATCTCCCGCCAAAGATATGGCC
 AACCACCAAGACCGCCAGCATCACTCTCGCAACAACTCCCAACACTCTAAGGCACTTCAAGGACAGGGCCCTGA
 GGACACACTGTTCTATTTGAACAACAGAGATTATTCACCGAATTAAGTGTCAACATTGCGCTCGGGGCGCTC
 GCTCCTCTTCTCCTACTTCTAGCTTTTGGCGGCTGTACTACAAAAAGCAACAGGCGCCATGAGACATGAGACATG
 GCGCCCGGATCCCCAGAGAAACACCAAAATGATATCGCTCATCCAGAACAGAGAGATCATGTCTCTGAGAT
 GAAGCAGCTGGAAACAGATCACGATCACGAGTGTGATCGCTGACAGCAACAGCACTCAGGCTCACCTGCCCCCAGA
 CTACACCTTACGCTGCGCGGTGCGCAGATGACATCCCACTTATGACGCCAAACACCATCACTGATTTCAA
 CACACTGACGGGATGACGCTTTGCCACTTTTAAACACTTCAGTGGAGCAAAACAGTACAAATTTACCCCA
 CGGACATTCCACCACTAGAGTATAGCTTTGCGCTATTTCCCTTCCCTATCTCTGCTCCCTACCGCTCAGCAACAT
 AGAAGAGGAGGAAAGAGAGAGGAAAGAGAGAGAGAGAAAGATCTCCAGACAGGAAATGTTTTTGTCCCACT
 GACTTAAAGACAAAATGCAAAAAGGCGAGTCATCCCATCCCGCAGACCCCTTATCGTGGTGTTTCCAGTATTAC
 AAGATCAACTTCTGACCCTGTGAAATGTGAGAAGTACACATTTCTGTTAAAAATACTGTCTTAAAGATCTCTACCA
 CTCCAACTCAATGTTTGTGTGATAGGACATCACTTTCAAGGCCCGGGTGTTCACAGCTCATGGAAGCAGCT
 GACACTCTTGAACCTCAGCGAAGGACACTTGATATTTTAAATTAACATGGAAGTTTAAACATGTTCTTCTGTGCG
 CACACATGATGGCTCTCTTAAAGTGAAGAAAGAGTCAATGAGATTTTCCCGCAGCATGGAGCTGTAATCCAG
 AGAGAGGAACCTGAGAAATTTATTTAAAGAGATGGACTGTGACGCGAAATCTGTACGGTTCTGTGCAAGAG
 GTGTTTGGCAGCTGAACATATTTTAAAGAGACTTGT

0976564-10160

FIGURE 151

MLNSVLLWLTALA IKFTLIDSSQAQYPVVNTNYGKIRGLRTPLPNEILGPVEQYLGVPYASP
PTGERRFQPEPPSSWTGIRNTTQFAAVCPQHLDERSLLHDMLPWFATANLDTLMTYVQDQN
EDCLYLNIIYVPTEDGANTKKNADDITSNDRGEDEDIHDQNSKKPVMVYIHGGSYMEGTGNMI
DGSILASYGNVIVITINYRLGILGFLSTGDQAAKGNYGLLDQIQALRWIEENVGAFGGDPKR
VTIFGSGAGASCVSLLTLSHYSEGLFQKAI IQSGTALSSWAVNYQPAKYTRILADKVGCNML
DTTDMVECLRNKNYKELIQQTITPATYHIAFGPVIDGDVIPDDPQILMEQGEFLNYDIMLGV
NQEGELKFVDGIVDNE DGVTPNDFDFSVSNFVDNLYGYPEGKDTLRETIKFMYTDWADKENP
ETRRKTLVALFTDHQWVAPAVAADLHAQYGSPTYFYAFYHHCQSEMKPSWADSAHGDEVPIV
FGIPMIGPTL FSCNFSKNDVMLS AVVMTYWTNFAKTGDPNQVPVQDTKFIHTKPNRFEEVA
WSKYNPKDQLYLHIGLKPRVRDHYRATKVAFWLELVPHLHNLNEIFQYVSTTTKVPPPDMTS
FPYGTRRSPAKIWPTTKRPAITPANNPKHSDPHKTGPEDTTVLIETKRDYSTELSVTI AVG
ASLLFLNILAFAALYYKKDKRRHETHRRRSPQRNTTNDIAHIQNEEIMSLQMKQLEHDHECE
SLQAHTLRLTCCPPDYTLTLRRSPDDIPLMTPTNTITMI PNTLTGMQLHTFNTFSGGQNSTN
LPHGHSTTRV

Signal sequence:

amino acids 1-24

Transmembrane domains:

amino acids 189-204, 675-692

FIGURE 152

GGGAAAGATGGCGGCGACTCTGGGACCCCTTGGGTCGTGGCAGCAGTGGCGGCGATGTTTGT
CGGCTCGGGATGGGTC CAGGATGTTACTCCTTCTTCTTTTGTGGGGTCTGGGCAGGGGCCA
CAGCAAGTCGGGGCGGGTCAAACGTT CGAGTACTTGAAACGGGAGCACTCGCTGTCGAAGCC
CTACCAGGGTGTGGGCACAGGCAGTTCCTCACTGTGGAATCTGATGGGCAATGCCATGTTGA
TGACCCAGTATATCCGCCTTACCCAGATATGCAAAGTAAACAGGGTGCCCTTGTGGAACCGG
GTGCCATGTTTCTCGAGAGACTGGGAGTTGCAGGTGCACCTTCAAATCCATGGACAAGGAAA
GAAGAACTCTGCATGGGGATGGCTTGGCAATCTGGTACACAAGGACTCGGATGCAGCCAGGGC
CTGTGTTTGGAAACATGGACAATTTGTGGGGCTGGGAGTATTTGTAGACACCTACCCCAAT
GAGGAGAAGCAGCAAGAGCGGGTATTCCCTCATCTCAGCCATGGTGAAACAACCGGCTCCCT
CAGCTATGATCATGAGCGGGATGGGCGGCCCTACAGAGCTGGGAGGCTGCACAGCCATTGTCC
GCAATCTTCATTACGACACCTTCTTGGTGATTGCTACGTCAAGAGGCAATTTGACGATAATG
ATGGATATTGATGGCAAGCATGAGTGGAGGGACTGCATTGAAGTGCCCGAGTCCGCCTGCC
CCGCGGCTACTACTTCGGCACCTCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCA
TTTCCTTGAAGTTGTTTGAACGTGACAGTGGAGAGAAACCCAGAGAGGAAAAGCTCCATCGA
GATGTGTTCTTGCCCTCAGTGGAACAATGAAGCTGCCTGAGATGACAGCTCCACTGCGGCC
CCTGAGTGGCCTGGCCCTTCTTCTCATCGTCTTTTTCTCCTGGTGTTTCTGTATTTGCCA
TAGTCATTGGTATCATACTCTACAACAAATGGCAGGAACAGAGCCGAAAGCGCTTCTACTGA
GCCCTCTGCTGCCACCACTTTTGTGACTGTACCCATGAGGTTATGGAAGGAGCAGGGCACTG
GCCTGAGCATGCAGCCTGGAGAGTGTCTTGTCTCTAGCAGCTGGTTGGGACTATATTCTG
TCACTGGAGTTTGAATGCAGGGACCCCGCATTCCTATGGTTGTGCATGGGGACATCTAACT
CTGGTCTGGGAAGCCACCCACCCAGGGCAATGCTGCTGTGATGTGCCTTTCCCTGCAGTCC
TTCCATGTGGGAGCAGAGGTGTGAAGAGAATTTACGTGGTTGTGATGCCAAAAACACAGA
AGAATTTCATAGCCAGGCTGCGCTGTTGTTTGAAGGAGGCTTCTACTTCAAGTTTGT
AATCCACAAGAATTAAGAACTGGTAACACACAGGCTTCTGACCATCCATTCTGTTGGGTT
TTGCATTTGACCCAAACCTCTGCTTACCTGAGGAGCTTCTTGTGAAACAGGATGGAAACT
TCTTCCCTGCTTACCTTCTTCACTCCATTCAATGTCTCTCTGTGTGCAACCTGAGCTG
GGAAAGGCATTTGGATGCCTCTCTGTTGGGGCTGGGGCTGCAGAACACACCTGCGTTTCA
TGGCCTTCATTAGGTGGCCCTAGGGAGATGGCTTCTGCTTGTGATCACTGTTCCCTAGCAT
GGGCTTGGGTCTATTGGCATGTCCATGGCCTTCCCAATCAAGTCTCTTCAGGCCCTCAGTG
AAGTTTGGCTAAAGGTTGGTGTAAAAATCAAGAGAAGCCTGGAAGACATCATGGATGCCATG
GATTAGCTGTGCAACTGACCACTCCAGGTTTGTGATCAAAACCAAAGCAACATTTGTGATGTG
GTCTGACCATGTGGAGATGTTTCTGACTGTCTAGAGCCTGCTTGTGCTGATGTTTGTAGT
TAGCATTTTGTGAATCCCACTTTGAGTGCTGAAAGTGAAGGAAGCTTCTTCTTACACCTT
GGCTTGGATATTGCCAGAGAAGAAATTTGGCTTTTTTTTCTTAATGGACAAGACAGT
TGCTGTTCTCATGTTCCAGTCTGAGAGCAACAGCCCTCATCTGTGCTCGGAGAGGTT
CACTGTCAATTGAGCAGCAGCAGCTGAGTGTGCGCTCTGTCAACCCCTTATTCCATGCTTCA
TTTGACAAGGGTTACATGCTGCTCACCTTATGCGCTGGGATTAAGTCAAGTTACAGGCCAG
AGTCTCCTTGGAGGGCTTGGAACTCTGAGTCTCTCTATGAACCTCTGTAGCCTAAATGAAT
TCTTAAATCACCAGTGGAAACAAAAAAGGGCGCCGCGACTCTAGAGTGC
ACCTGCAGTAGGATAACAGGGTAATAAGCTTGGCGCCATG

097854-101601

FIGURE 153

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911
><subunit 1 of 1, 348 aa, 1 stop
><MW: 39711, pI: 8.70, NX(S/T): 1
MAATLGPLGSWQQWRRCLSDGSRMLLLLLLLGSGQGPGQVGAGQTFEYLKREHSLSKPYQ
GVGTGSSSLWNLMGNAMVMTQYIRLTPDMQSKQGALWNRVPCFLRDWELQVHFKIHGQGKKN
LHGDGLAIWYTKDRMQPGPVFGNMDKFVGLGVFVDITYPNEEKQQERVFPYISAMVNNGSLSY
DHERDGRPTELGGCTAIVRNLYHDTFLVIRYVKRHLTIMMDIDGKHEWRDCIEVPGVRLPRG
YYFGTSSITGDLSDNHVISLKLFEFTVERTPEEEKLHRDVFPLPSVDNMKLPENTAPLPPLS
GLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRKRFY

Signal sequence:

amino acids 1-38

Transmembrane domain:

amino acids 310-329

00978564.101001

FIGURE 154

CCGAGCCGGGCGCGCAGCGAGCGAGCTGGGGCCGSCCTGGGACCATGGGCGTGAGTGCAATCTACGGATCAGTCT
 CTGATGGTGGGTCGTAACTCAGTGGGGATCCCAAGATTCCATGAAGAAAATCAGTGTCTCTCATTCAAGAAAT
 TGGGCTCTGGCTCAGAATTCCTGCAGCTGGTGAAATCTGTTTCTAGAAGAGGTTTAAATTAATGCCTCAGTCT
 GACATGTTCCCGATTGTAGGTGAAACCATGAAGAGAAAAAGAAATCTTAATATATGCTTTTCCGCAACCGCTCT
 TGCTGTGCTGGCCCTGGCTGCGCTGCTGGCCCTTTGTGAGCCTCAGCCTCAGGTTCTTCCACCTGATCCCGGTGT
 CGACTCTCAAGAATGGAATGAGTAGCAAGAGTGCAGAGAGAAATCATGCCCGACCTGTGAACGGAGCCCCCTGTGA
 CAGACCCCGCTTTATGAAGCTTTTGTGATCTGCAACATCCCGAGTGGCCGAGCGCAGCATGGAAGGTGATGCGCC
 CGCATCATTTTAAAGTGTCTCAGTGCATGTGTTTATTCGCAACGAGAGCAGGTACCCACTGTATGTCTATCCCA
 AACAAGCGGACCAAGAAATTCAGTGCACCTCTGGTGGCTAACAGGAAACCGTATCAACCCAAAATCGGAAGCTTTCA
 TTAGTACATGTTCAAAAGGATCCGGAGCCTCTTTGCAAGCCCTTGAACCTCTTGGCTCTTTACCCAAATCACC
 CATTGTGTAGATGGGAGACTCACAAGACAGGAGTTGTGCGACATTTGCAAGACCGTGTGAGGAGGATTA
 TCTATCTAAAGAAACAAACATCTCTGCCAATGATTGGTCTGCGACACAGCTCTATTATAGAGACCACTGGGAAAA
 GCCGAGCCCTACAAGTGGGCTGGCTTCTGCTTTATGGCTTTCTCCAGATTTTGACTGGAAGAAATTTATTTC
 GGCACACGCTCAAGTGGCTGTTCTGCTCTGGAAGCTGCTATTGCCCCGTTAAGAAACCAAGTATCGGAAGAGGAGC
 AGCGTCGTGATGCTTCTACGTTTGA AAAACAGCCAGCTGGAGAAAGCCTACGCGGAGATGGCCCAAGATCGTGG
 ATGTCGCCCAAGCAGCTTAGAGTGCACCAACCCATAGACTCCATGCTCTGCCACTTCTGCCCAATGTGACGT
 TTCCTGTACCAAGAAATGGCTGTGTTGACATGGAGCACTCAAGGTAATTAAGACCCATCAGATCGAGGATGA
 GGGAAAGACGGGAGAAAGAAATGTACTTCCGGTATTCTCTCTGGGTGCCACCCCATCTGAACCAAAACATCG
 GCCGATGACGCGTGCCACAGAGGCGAGAAAGAGGCTCTTGGCCCTACTCTGCTCATGTATGCTCACTCTGT
 CACAGTTTCTCAGTGGCTTGGCCCTTTCAGAAGCCAGGTTCCCAAGGTTTGCAGCCAGGTTGATCTTTGAGCTTT
 GGCAGACAGAGAAACCCAGTGAACATTCGCTCCGATTTCTTAAGAGGGTTCAGATGTCACATTCACACT
 CTTTCTGCCAAGACCAACAAGCGTTCTCCCAAGCCCATGTGCCCGCTTGAACACTTGGTCGCTTTGTGAAAA
 GGGACATGTTTGTAGCCCTGGGTGGCAGTGGTACAAATTTATTATGATGCATGTCTACAGGGAAGGATTTAAAGG
 TATGCGATCAGCAGTATAGAATCCATGCCAATACAGAGCATAGGGAAGGTCCTCTGATTTTGTCTGTTAC
 TAAGGGTAAAGATTTATGCTTTTAAAGGCTAAATATTGTTTGTGGGAACCATGATGTTGGGGTTGAACAGT
 AAGCATTTGCTGCAATGTGGTACGTGAATTTGCTTGGTACAAAATGGCCAGTTACAGAGGAATAGAAGGTACTT
 TATCATAGCCAGACTCTGCTTAGAATGCCAGAAATATATAGTTCAAGACCTGAAGTTGCCAATCCAAGTTTGCAC
 TCTCTGGCGCTGCCCATGTTACTATGTGATGGAACAGCACAACCTCAACCAAAATTTTAAATCTTAGACATT
 TTTACCTTGTCTGTTTGAAGAATTTCTTGAAGTGAATTTATCTAAAATTAAGGTTGGCAAACTTTTCTGTAAAGG
 GCCGATTGTAAATATTTTCAGACTGTGTGGACCAAAAGGCCACATACAGTCTCTGTCTAAACTACTCAACTCTGT
 TTTCTGAAGCAGGAAAGCCACCAAGACAGTACATTAAGGAATATGTGTAGCTGGGTCCCGAGCCAGACAAAACA
 GATGGTGACCAAGCTTGGCCCTGGGCTGTAGTTTGTGACCCCTCATCTAAAATAAGGCTATACATAAATTGC
 ACTTCCAGCACTTTGAGAACGAGTTGAATACCAAGAAATTTCAATGGTTCTCCAGTAACCTTCTGTGAGAAACA
 CAGAATTTGGTCTGATCTGACACTAGAACA AAAACTTGAGGGTAAATAAACAATTTGAATTAGAATGAATCATAGAA
 AACTGATTAGAAGAATCTTGTAGTTTATGATGATTGTGGTCAAGATAGTTTAAAGTATGTTCTAAATATTGTT
 TTTCTAGTAGTCTATTTGCTGTATATGCTGAAATTTTGTATGCCATTTAGTATTTTATGTTTAGGAAAAATTT
 TTTCTAAGACCAGTTTGTAGTACTCTTATCTCTGTAGTAATATTTCAATTTGGCTGTACCTGCTTGGTGGTTAGAA
 ACTGGATTCTATTTTAAACCAATTTTCATAGTTTCAAAATGGTAAATTTCTGATTGATTTTAAATGCGTTTGTGA
 AGAAGCTTTGCTATTAGGTAGTTTACAGATCTTTATAAGGTGTTTATATATTAAGAGCAATATAAATATCATCTG
 TGATTTCTGAAGCAATGTGCTCAATTCAGAGAAATGGAAGGTGAAAGTGAGATTCTCTGTTGTCTATCGGCATTCC
 AACTTTTCTCTGTTTGTGTTCCAGTGTGCAATTTGAATATGCTGTTCTATATAATAGATTTTAAAGAAATA

09978564.10460

FIGURE 155

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329
><subunit 1 of 1, 480 aa, 1 stop
><MW: 55240, pI: 9.30, NX(S/T): 2
MLFRNRFLLLLALAAALLAFVSLSLQFFHLIPVSTPKNGMSSKSRKRIMPDPVTEPPVTDVPVY
EALLYCNIPSPAERSMEGHAPHHFKLVSVHVFIRHGDYPLYVIPKTKRPEIDCTLVANRKP
YHPKLEAFISHMSKSGSGASFESPLNSLPLYPNHPLCEMGELTQTGVVQHLQNGQLLRDIYLK
KHKLLPNDWSADQLYLETTGKSRTLQSGLALLYGFLPDFDWKKIYFRHQPSALFCSGSCYCP
VRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSM LCHFCHNVSFPC
TRNGCVDMEHFKVIKTHQIEDERERREKKLYFGYSLLGAHPILNQITIGRMQRATEGRKEELF
ALYSAHDVTLSPVLSALGLSEARFPRFAARLIFELWQDREKPSSEHSVRILYNGVDVTFHTSF
CQDHHKRSPPKMCPLNLVRFVKRDMFVALGGSGTNYDACHREGF

Signal sequence:

amino acids 1-18

09978554-101601

W. H. B. & Co. Ltd.

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><subunit 1 of 1, 916 aa, 1 stop
```

><MW: 100204, pI: 4.92, NX(S/T): 4

Signal sequence:

amino acids 1-30

Transmembrane domains:

amino acids 693-711, 809-823, 869-888

FIGURE 158

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCAGTTAAAAG
GCTCCAGAATCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAA
TCAGTAGGTGACCCCGCCCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCCGACCTCGT
GCGGCCAAGACGTGGATGTTCTTGCTCTTGCTGGGGGAGCCTGGGCAGGACACTCCAGGGC
ACAGGAGGACAAGGTGCTGGGGGGTCATGAGTGCCAAACCCATTGCGAGCCTTGGCAGGCGG
CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGAGGTGGCAACTGGGTCTT
ACAGCTGCCCACTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTACAGAA
TAAAGATGGCCAGAGCAAGAAATACCTGTGGTTCAGTCCATCCACACCCCTGCTACAACA
GCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCC
CTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTG
CACCGTCTCAGGCTGGGGCACTGTCACCAGTCCCGAGAGAATTTTCCTGACACTCTCAACT
GTGCAGAAGTAAAAATCTTTCCTCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACA
GATGGCATGGTCTGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGG
CCCCCTGGTGTGTGATGGTGCACTCCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGA
GGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATC
ATAGGCAGCAAGGGCTGAATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACCTCT
CTGGTTC

097854 10464
104101-4958/660

FIGURE 159

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48336
<subunit 1 of 1, 260 aa, 1 stop
<MW: 28048, pI: 7.87, NX(S/T): 1
MGRPRPRAAKTWMLLLLGGAWAGESRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVL
VGGNWLTAAHCKPKYTVRLGDHSLQNKDGPEQEIPVVQSI PHPCYNSSDVEDHNHDLMLL
QLRDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFDTLNCABVKIFPQKKCED
AYPGQITDGMVCAGSSKGADTCQGDSGGPLVCDGALQGITSWGS DPCGRSDKPGVYTNICRY
LDWIKKIIGSKG

Important Features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 51-71

N-glycosylation site.

amino acids 110-113

Serine proteases, trypsin family, histidine active site.

amino acids 69-74 and 207-217

Tyrosine kinase phosphorylation site.

amino acids 182-188

Kringle domain proteins motif

amino acids 205-217

109101-4958/66

FIGURE 160

GGCGCCGGTGCACCGGGCGGGCTGAGCGCCTCCTGCGGCCCGGCGCTGCGCGCCCCCGGCCCGC
CGCGCCGCCACGCCCCAACCCCGGCCCGCGCCCCCTAGCCCCCGCCCGGGGCCCGCGCCCGC
GCCCGCGCCAGGTGAGCGCTCCGCCCGCGCAGGCCCCGCCCGGCCCGCCCGCCCGCCCGC
CCCCGGCCGGCGGGGAACCGGGCGGATTCTCGCGCGTCAAACCACTGATCCCCATAAAAC
ATTATCTCTCCCGGGCCCGCGCTGCGAGCGCCCCGCCAGTCCGCGCCGCCCGCCCTCG
CCCTGTGCGCCCTGCGCGCCCTGCGCACCCCGGCCCGAGCCCCAGCCAGAGCCGGGCGGAGC
GGAGCGCGCCGAGCCTCGTCCCGCGGCCGGGCGGGGCCGGGCGGTAGCGCGCGCCCTGGA
TGGCAGACCCGGCCGGGGGAGACGGGCGCCCGCCGAAACGACTTTTCAGTCCCGCAGCGCGC
CCCGCCCAACCCCTACGATGAAGAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTG
CTGTGGCTGCAGGCCCTGGCAGGTGGCAGCCCCATGCCAGGTGCTGCGTATGCTACAATGA
GCCCAAGGTGACGACAAGCTGCCCCAGCAGGGCCCTGCAGGCTGTGCCCGTGGGCATCCCTG
CTGCCAGCCAGCGCATCTTCTGCAACGGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTC
CGTGCCTGCCCAACCTCACCATCTGTGGCTGCACTCGAATGTGCTGGCCCGAATTGATGC
GGCTGCCTTCACTGGCCCTGGCCCTCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCC
GGTCTGTGGACCTTGCACATTCCACGGCCTGGGCGCGCTACACACGCTGCACCTGGACCGC
TGCGGCCCTGCAGGAGCTGGGCCCCGGGGCTGTTCGCGGCCCTGGCTGCCCTGCAGTACCTTA
CCTGCAGGACAACCGCGCTGCAGGCACTGCCTGATGACACCTTCCGCGACCTGGGCAACCTCA
CACACCTCTTCTGCAGGGCAACCGCATCTCCAGCGTGCCCGAGCGCGCCTTCCGCTGGGCTG
CACAGCCTGCACCGCTCTCTACTGCACCAAGAACCGCGTGCGCCATGTGCACCCCGCATGCCTT
CCGTGACCTTGGCCGCTCATGACACTCTATCTGTTTGCCAAACAATCTATCAGCGCTGCCCA
CTGAGGCCCTGGCCCCCTGCGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTG
TGTGACTGCCGGGCACGCCCACTCTGGCCCTGGCTGCAGAAGTTCCCGGGCTCCTCCTCCGA
GGTGCCCTGCAGCCTCCCGCAACGCCCTGGCTGGCCGTGACCTCAAACGCCCTAGCTGCCAATG
ACCTGCAGGGCTGCGCTGTGGCCACCGGCCCTTACCATCCCATCTGGACCGCGAGGGCCACC
GATGAGGAGCCGCTGGGGCTTCCCAAGTGCTGCCAGCCAGATGCCGCTGACAAGGCCCTCAGT
ACTGGAGCCTGGAAGACCAGCTTCGCGAGGCAATGCGCTGAAGGGAGCGGTGCCGCCCGGTG
ACAGCCCGCGGGCAACGGCTCTGGCCACGGCAATCAATGACTCACCCTTTGGGACTCTG
CCTGGCTCTGTGAGCCCCGCTCACTGCAGTGCAGGCCGAGGGCTCCGAGCCACAGGGTT
CCCCACCTCGGGCCCTCGCCGGAGGCCAGGCTGTTACGCAAGAACCAGCACCCCGAGCCACT
GCCGTCTGGGCCAGGCAGGCAGCGGGGTGGCGGGACTGGTGACTCAGAAGGCTCAGGTGCC
CTACCCAGCCTCACCCTGACGCTCACCCTTGGCCCTGGCGCTGGTGCTGTGGACAGTGCT
TGGGCCCTGCTGAACCCAGCGGACACAAGAGCGTGCTCAGCAGCAGGTGTGTGTACATAC
GGGGTCTCTCTCCACGCCGCAAGCCAGCCGGGCGGCCGACCCGCTGGGGCAGGCCAGGCCAG
GTCCTCCTGTAGGACGCTCGCCCGGCCACCCCATCTCCACCCCATCATGTTTACAGGG
TTCCGGCGGACGCGTTTGTTCAGAACGCGCTCCACCCAGATCGCGGTATATAGAGATAT
GCATTTTATTTTACTTGTGTAAAAATATCGGACGAGCTGGAATTAAGAGCTCTTTTCTTAA
AAAA

09973564.1160

FIGURE 161

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44184
><subunit 1 of 1, 473 aa, 1 stop
><MW: 50708, pI: 9.28, NX(S/T): 6
MKRASAGGSRLLEAWLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVFVGIPAASQRI
FLHGNRISHVPAASFRACRNLTLWLHSNVLARIDAAFTGLALLEQLDLSDNAQLRSVDPA
TFHGLGRHLHTLHLDRCGLQELGPGLFRLGALQYLYLQDNALQALPDDTFRDLGNLTHLFLH
GNRISSVPERAFRGLHSLDRLLHQNVRVAHVHPHAFRDLGRMLTYLYLFANNLSALPTEALAP
LRLQYLRRLNDNPWVCDRCARPLWAWLQKFRGSSSEVPCLPQRLAGRDLLKRLAANDLQGCA
VATGPHYPIWTGRATDEEPLGLPKCCQPDAAADKASVLEPGRPASAGNALKGRVPPGDSPPGN
GSGPRHINDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLLGQA
GSGGGTGDSESGALPSLTCSLTPLGLALVLWTVLGPC

Important features:

Signal peptide:

amino acids 1-26

Leucine zipper pattern.

amino acids 135-156

Glycosaminoglycan attachment site.

amino acids 436-439

N-glycosylation site.

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

WWFC domain

amino acids 411-425

FIGURE 162

GGAAGTCCACGGGGAGCTTGGATGCCAAAGGGAGGACGGCTGGGTCTCTGGAGAGGACTAC
TCACTGGCATATTTCTGAGGTATCTGTAGAATAACCAAGCTCAGATACTGGGGACCTTTAC
AGTCCCACAGAAACCGTCTCCAGGAAGCTGAATCCAGCAAGAACAATGGAGGCCAGCGGGA
AGCTCATTTGCAGACAAAGGCAAGTCTTTTTTCTCTTTTGGGCTTATCTCTGGCG
GGCGCGCGGAACCTAGAAGCTATTCTGTGGTGGAGGAACTGAGGGCAGCTCCTTTGTCTAC
CAATTTGGCAAAGGACCTGGGTCTGGAGCAGAGGGAATTCTCCAGCGGGGGGTTAGGGTTG
TTTCCAGAGGGAAACAACTACATTTGCAGCTCAATCAGGAGACCGCGGATTGTTGTCTAAAT
GAGAATTTGACCGTGAGGATCTGTGCGGTCAACAGAGCCCTGTGTGCTACGTTTCCAAGT
GTTGCTAGAGAGTCCCTTCGAGTTTTTTCAAGCTGAGCTGCAAGTAATAGACATAAAGCACC
ACTCTCCAGTATTTCTGGACAAACAAATGTTGGTGAAAGTATCAGAGAGCAGTCTCTCTGGG
ACTACGTTTTCTCTGAAGAATGCCGAAGACTTAGATGTAGGCGAAACAATATTGAGAACTA
TATAATCAGCCCCAATCTCTATTTTCGGGTCTCTACCCGCAACAGCAGTGATGGCAGGAAAT
ACCCAGAGCTGGTGCTGGACAAAGCGCTGGACCGAGAGGAAGAAGCTGAGCTCAGGTTAAACA
TCTCAGCACTGGATGGTGGCTCTCCGCCAGATCTGGCACTGCTCAGGTCTACATCGAAGT
CCTGGATGTCAACGATAATGCCCTTGAATTTGAGCAGCCTTTCTATAGAGTGCAGATCTCTG
AGGACAGTCCGTAGGCTTCTCTGGTTGTGAAGGTCTCTGCCACGGATGTAGACACAGGAGTC
AACGGAGAGATTTCTATTCACTTTTCCAAGCTTCAAGAAGAGATTGGCAAACCTTTAAGAT
CAATCCCTTGACAGGAGAAATTTGAAGTAAAAAACAACCTCGATTTCGAAAAAATCTCAGTCT
ATGAAGTCAATATTGAGGCAAGAGATGCTGGAACCTTTCTGGAATAATGCACCGTTCTGATT
CAAGTGATAGATGTGAACAGCATTGCCCCAGAAAGTTACCATGTCTGCATTTACCAGCCCAAT
ACCTGAGAACCGCGCTGAAATCTGTGGTTGCACTTTTCAGTGTTTCAGATCTTGATTTCAGGAG
AAAATGGGAAAAATTAGTTGCTCCATTTCAGGAGGATCTACCTTCTCTGAAATCCGCGGAA
AACTTTTACACCTACTAACGGAGAGACCACTAGACAGAGAAAGCAGAGCGGAATACAACAT
CACTATCACTGTCACTGACTTGGGACCCCTATGCTGATAACACAGCTCAATATGACCGTGC
TGATCGCCGATGTCAATGACAACGCTCCCGCCTTCACCCAAACTCCTACACCCGTGTTCCGTC
CGCGAGAACACAGCCCCCGCCTGACATCCGACGCGTCAAGCGCTACAGACAGAGACTCAGG
CACCAACGCCCGAGGTCACTTCTCGTGTCCGCCCCAGGACCCGCACTGCCCTCAGAT
CCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTCCGCCCTCAGGTCTCTGGACTACGAG
GCCGTGACGGGGTTTCAAGTTCCGCTGGCGCTTTCAGACCACGGCTCCCCGGCGCTGAGACG
CGAGGCGCTGGTGCGCGTGGTGGTGTGTTGAGCGCCAACGCAACTCGCCCTTCGTGCTGTACC
CGCTGCAGAACGGCTCCGCGCCTGACACCGAGCTGGTGCCCGGGCGCGGAGCCGCGGTAC
CTGGTGACCAAAGGTGGTGGCGGTGGAACGGCGACTCGGGCCAGAACGCTGGCTGTGCTAGCA
GCTGCTCAAGGCCACGGAGCTCGGTCTGTTCCGCGTGTGGGCGCACAATGGCGAGGTGCGCA
CCGCCAGGCTGCTGAGCGAGCGGACGCGCGGCAAGCACAGGCTGGTGGTGTGTTCAAGGAC
AATGGCAGGCTCTCGCGCTCGGCCACCGCCACGCTGCACGTGCTCTCTGGTGGACGCGCTTCTC
CCAGCCCTACCTGCGCTCTCCCGGAGGCGGCCCCGACCCAGGCCAGGCCGACTTGCTACCGG
TCTACCTGGTGGTGGCGTTGGCCCTCGGTCTTCTGCTCTTCTCTTTCCGTGCTCCTGTTCT
GTGGCGGTGCGGCTGTGTAGGAGGAGCAGGGCGGCTCGGTGGGTGCTGCTTGGTGCCCGA
GGGCCCCCTTCAGGGCATCTGTGGACATGAGCGGCACAGGACCCCTATCCAGAGCTACC
AGTATGAGGTGTGCTCGGAGGAGGCTCAGGGACCAATGAGTTCAAGTTCCATGAGCCGATT
ATCCCCAACTTCCCTCCCAAGTGCCCTGGGAAAGAAATACAAGGAAATCTACCTTCCCCAA
TAACCTTGGGTTCAATATTTCAGTGCATAGTTGACTTTTACATTCCATAGGTATTTTATT
TGTGGCATTTCCATGCCAATGTTTATTTCGCCCAATTTGTGTGATGTAAATTTGTAGCGGAT
TTACTCTTGATTTTTCTCATGTTCTTCTCCCTTTGTTTTAAAGTGAACATTTACCTTTATT
CCTGGTTCTT

FIGURE 163

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48314
<subunit 1 of 1, 798 aa, 1 stop
<MW: 87552, pI: 4.84, NX(S/T): 5
MEASGKLIQRQVLFSPFLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEQREFSR
RGRVRSVSRGNLHLQLNQETADLLNEKLDREDLCGHTEPCVLRVQVLESFFEFFQAEQV
IDINDHSPVFLDKQMLVKVSESSPPGTTTFPLKNAEDLDVGQNNIENYIISPNSYFVLTRKR
SDGRKYPELVLDKALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVLDVNDNAPEFEQPFY
RVQISEDSPVGFLVVKVSATDVTGTVNGEISYSLFQASEEIGKTFKINPLTGEIELKKQLDF
EKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAPVETMSAFTSPIENAPETVVALFSVS
DLDSGEGNKISCSIQEDLPFLLKSAENFYTLTERPLDRESRAEYNITITVTDLGTPLITQ
LNMTVLIADVNDNAFAFTQTSYTLFVRENNSPALHIRSVSATDRDSTNAQVTYSLLPPQDP
HLPLTSLVSNADNGHLFALRSLDYALQGFQFRVGASDHGSPALSSSEALVRVVLDANDNS
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATELGLFGVNAH
NGEVRTARLLSERDAAKHRLVLVLVDKNGEPPRSATATLHVLLVDGFSQPYLPLPEAAPTQAO
ADLLTVYLVVALASVSSSLFSLFVLLFVAVRLCRRSRAASVGRCLVPEGPLPGHLVDMSGTRT
LSQSYQYEVCLAGGSGTNEFKFLKPIIPNPPQCPGKEIQGNSTFPNNFGFNIQ

Important features:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 685-712

Cadherins extracellular repeated domain signature.

amino acids 122-132, 231-241, 336-346, 439-449 and 549-559

ATP/GTP-binding site motif A (P-loop).

amino acids 285-292

N-glycosylation site.

amino acids 418-421, 436-439, 567-570 and 786-789

097355.101601

FIGURE 164

ACCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCGCTAGCCGTGC
GCCGATTGCTCTCGGCCCTGGGCAATGCTCCGGCTGCCGCTCGACGACCGCCCGCGTCAT
GCGGCTCCTCGGCTGGTGGCAAGTATTGCTGTGGGTGCTGGGACTTCCCGTCCGCGCGGTGG
AGGTTGCAGAGGAAAGTGGTCGCTTATGGTCAGAGGAGCAGCCTGCTCACCTCTCCAGGTG
GGGGCTGTGTACCTGGGTGAGGAGGAGCTCCTGCATGACCCGATGGGCCAGGACAGGGCAGC
AGAAGAGGCCAATGCGGTGCTGGGGCTGGACACCCAGGCGATACATGGTGATGCTGTCTG
TGATTCTGGGGAAGCTGAGGACAAAGTGAGTTCAGAGCCTAGCGGCGTCACTGTGGTGCT
GGAGGAGCGGAGGACTCAAGGTGCAACGTCCGAGAGAGCCTTTTCTCTCTGGATGGCGCTGG
AGCACACTTCCCTGACAGAGAAGAGGAGTATTACACAGAGCCAGAAGTGGCGGAATCTGACG
CAGCCCCGACAGAGGACTCCAATAACA CTGAAAGTCTGAAATCCCCAAAGGTGAACTGTGAG
GAGAGAAACATTACAGGATTAGAAAAATTTCACTCTGAAATTTTAAATATGTACAGGACCT
TATGGATTTTCTGAACCCAAACGGTAGTGACTGTACTCTAGTCTGTGTTTACACCCCGTGGT
GCCGCTTTTCTGCCAGTTTGGCCCCCTCACTTTAACTCTCTGCCCCGGGCATTTCCAGCTTT
CACTTTTGGCACTGGATGCATCTCAGCACAGCAGCCTTTCTACCAGGTTTGGCACCGTAGC
TGTTCTAATATTTTATTATTTCAGGAGCTAAACCAATGGCCAGATTTAATCATAACAGATC
GAACACTGGAACACTGAAAACTTTCATTTTAAATCAGACAGGTATAGAAGCCAAGAAGAAT
GTGGTGGTAACTCAAGCCGACCAAAATAGGCCCTCTTCCAGCACTTTGATAAAAAGTGTGGA
CTGGTTGCTTGTATTTTCCTTATTCTTTTAAATAGTTTTATTATGTATGCTACCATTCGAA
CTGAGAGTATTGCGTGGCTAATTCCAGGACAAGAGCAGGAACATGTGGAGTAGTGATGGTCT
GAAAGAAGTTGGAAGAGGAACTTCAATCCTTCGTTTCAGAAATTAGTGCTACAGTTTCATA
CATTTTCTCCAGTGACGTGTTGACTTGAAACTTCAGGCAGATTAAAGAATCATTTGTTGAA
CAACTGAATGTATAAAAAAATTATAAACTGGTGTTTTAACTAGTATTGCAATAAGCAAATGC
AAAAATATTCAATAG

097654-101601

FIGURE 165

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48333
><subunit 1 of 1, 360 aa, 1 stop
><MW: 39885, pI: 4.79, NX(S/T): 7
MVPAAGRPPPRVMRLLGWWQVLLWVLGLPVRGVEVAEESGRLWSEEQPAHPLQVGAVYLGEE
ELLHDPMGQDRAAEEANAVLGLDTQGDHVMVLSVIPGEAEDKVSSEPSGVTGAGGAEDSRC
NVRESLFSLDGAGAHFPDREEEYYTEPEVAESDAAPTEDSNNTESLSPKVNCEERNITGLE
NFTLKILNMSQDLMDFLNPNGSDCTLVLFYTPWCRFSASLAPHFNSLPRAFPAHFLALDAS
QHSSLSTRFGTVAVPNILLFQGAKPMARFNHTDRTLETCLKIFIFNQTGIEAKKNVVVTQADQ
IGPLPSTLIKSVDWLLVFSLSFFLISFIMYATIRTESIRWLIPGQEHEVE

Important features:

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 321-340

Homologous region to dilsufide isomerase

amino acids 212-302

N-glycosylation site.

amino acids 165-168, 181-184, 187-190, 194-197, 206-209, 278-281
and 293-296

Thioredoxin domain

amino acids 211-227

0978564-101601

FIGURE 166

CCCGGCTCCGCTCCCTCTGCCCCCTCGGGGTCGCGCGCCACGATGCTGCAGGGCCCTGGCT
CGCTGCTGCTGCTCTTCTCGCCTCGCACTGCTGCCTGGGCTCGGCGCGGGGCTCTTCCCTC
TTTGGCCAGCCGACTTCTCTACAAGCGCAGCAATTGCAAGCCCATCCCGGTCAACCTGCA
GCTGTGCCACGGCATCGAATACCAGAACATGCGGGCTGCCCA^ΔCCTGCTGGGCCACGAGACCA
TGAAGGAGGTGCTGGAGCAGGCCGCGCTTGGATCCCGCTGGTCATGAAGCAGTGCCACCCG
GACACCAAGAAGTTCCTGTGCTCGCTCTTCGCCCCCGTCTGCCTCGATGACCTAGACGAGAC
CATCCAGCCATGCCACTCGCTCTGCGTGCAGGTGAAGGACCGCTGCGCCCCGGTCTGTCCG
CCTTCGGCTTC^ΔCCCTGGCCCGACATGCTTGAGTGCACCGTTTCCCCCAGGACAACGACCTT
TGCATCCCCCTCGCTAGCAGCGACCACTCCTGCCAGCCACCGAGGAAGCTCCAAAGGTATG
TGAAGCCTGCAAAAATAAAAAATGATGATGACAACGACATAATGGAACCGCTTTGTAAAAATG
ATTTTGCAC^ΔTGAAAAATAAAGTGAAGGAGATAACCTACATCAACCGAGATACAAAATCATC
CTGGAGACCAAGAGCAAGACCATTTACAAGCTGAACGGTGTGTCCGAAAGGGACCTGAAGAA
ATCGGTGCTGTGGCTCAAAGACAGCTTGCAAGTGCACCTGTGAGGAGATGAACGACATCAACG
CGCCCTATCTGGTTCATGGGACAGAAACAGGGTGGGGAGCTGGTGATCACCTCGGTGAAGCGG
TGGCAGAAGGGGCAGAGAGAGTTCAAGCGCATCTCCGCGAGCATCCGCAAGCTGCAGTGC^{TA}
^ΔTCCCCGGCATCCTGATGGCTCCGACAGGCCTGCTCCAGAGCACGGCTGACCATTCTGCTCC
GGGATCTCAGCTCCCGTTCCCCAAGCACACTCCTAGCTGCTCCAGTCTCAGCCTGGGCAGCT
TCCCCCTGCCTTTTGCACGTTTGCATCCCCAGCATTTCTGAGTTATAAGGCCACAGGAGTG
GATAGCTGTTTTACCTAAAGGAAAAGCCACCCGAATCTGTAGAAATATTCAAAC^ΔTAAATA
AAATCATGAATATTTTAA

FIGURE 167

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50920
><subunit 1 of 1, 295 aa, 1 stop
><MW: 33518, pI: 7.74, NX(S/T): 0
MLQGGPSLLLLFLASHCCLGSAAGLFLFGQPDFSYKRSNCKPIPVNLQLCHGIEYQNMRLPN
LLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAFVCLDDLDLDETIQPCHSKCVQVKDR
CAPVMSAFGFPWPDMLCDRFPQDNDLCIPLASSDHLLPATEEAPKVCEACKNKNDNDNDIM
ETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVLWLKDSLQCTCE
EMNDINAPYLVMGQKQGGLVITSVKRWQKGQREFKRISRIRKLQ

Important features:

Signal peptide:

amino acids 1-20

Cysteine rich domain, homologous to frizzled N terminus

amino acids 6-153

097864-10101

FIGURE 168

GTGGAGGCCGCCGACGATGGCGGGGCCGACGGAGGCCGAGACGGGGTTGGCCGAGCCCCGGG
CCCTGTGCGCGCAGCGGGGCCACCGCACCTACGCGCGCGCTGGGTGTTCTGTCTCGCGATC
AGCCTGTCTCAACTGTCTCCAACGCCACGCTGTGGCTCAGCTTTGCACCTGTGGCTGACGTCAT
TGCTGAGGACTTGGTCTGTCCATGGAGCAGATCAACTGGCTGTCACTGGTCTACCTCGTGG
TATCCACCCCATTTGGCGTGGCGGCCATCTGGATCCTGGACTCCGTCGGGTCCGTGCGGCG
ACCATCTCTGGGTGCGTGGCTGAACTTTGCCGGGAGTGTGTACGCATGGTGCCTGCGATGGT
TGTGGGACCCAAAACCCATTTGCCCTTCCTCATGGGTGGCCAGAGCCTCTGTGCCCTTGCCC
AGAGCCTGGTCACTTCTCTCCAGCCAAGCTGGCTGCCTTGTGGTTCCAGAGCACAGCGA
GCCACGGCCAACATGCTCGCCACCATGTGCAACCCCTCTGGGCGTCCTTGTGGCCAATGTGCT
GTCCCCCTGTGCTGGTCAAGAAGGGTGAGGACATTCCGTTAATGCTCGGTGTCTATACCATCC
CTGCTGGCGTCGTCTGCCTGTGTCCACCATCTGCCTGTGGGAGAGTGTGCCCCCCACCCCG
CCCTCTGCCGGGCTGCCAGCTCCACCTCAGAGAAGTTCTCGGATGGGCTCAAGCTGCAGCT
CCTCTGGAAACAAGGCTATGTCTATCCTGGCTGTGTGCTTGGGGGAATGATCGGGATCTCTG
CCAGCTTCTCAGCCCTCCTGGAGCAGATCCTCTGTGCAAGCGGCCACTCCAGTGGGTTTTCC
GGCCTCTGTGGCGCTCTCTTCATCACTTTGGGATCCTGGGGGCACTGGCTCTCGGCCCTTA
TGTGGACCGGACCAAGCACTTCACTGAGGCCCAAGATTGGCCTGTGCCCTGTTCTCTGTGG
CCTGCGTGCCCTTTGCCCTGGTGTCCAGCTGCAGGGACAGACCTTGCCCTGGCTGCCACC
TGCTCGCTGCTCGGGCTGTTTGGCTTCTCGGTGGGCCCCGTGGCCATGGAGTTGGCGGTGCA
GTGTTCCCTTCCCGTGGGGGAGGGGGCTGCCACAGGCATGATCTTTGTGTGGGGCAGGCCG
AGGGAATACTCATCATGTGGAATGACGGCACTGACTGTGCGACGCTCGGAGCCGTCCTTG
TCCACCTGCCAGCAGGGGGAGGATCCACTTGACTGGACAGTGTCTCTGCTGCTGATGGCCGG
CCTGTGCACCTTCTTTCAGCTGCATCCTGGCGGTCTTCTTCCACACCCCATACCGGCGCTGC
AGGCCGAGTCTGGGGAGCCCCCTCCACCCGTAAACGCGTGGGCGGCGCAGACTCAGGGCCG
GGTGTGGACCGAGGGGAGCAGGAAGGGCTGGGGTCTTGGGGCCAGCACGGCGACTCCGGA
GTGCACGGCGAGGGGGGCTCGCTAGAGGACCCAGAGGCCCGGGAGCCCCACCCAGCCT
GCCACCGAGCGACTCCCGTGCACAAGGCCAGCAGCCACCGACGCGCCCTCCCGCCCCGGC
AGACTCGCAGGCAGGGTCCAAGCGTCCAGTTTATTGACCCGGCTGGGTCTCACTCCTCCTT
CTCCTCCCCGTGGGTGATCAGCTAGCTGAGCGCCTTGTAGTCCAGGTTGCCCGCCACATCGA
TGGAGGCGAACTGGAACTCATCTGGTCCACCTGCGGGCGGGGGCGAAAGGGCTCCTTGGGGCT
CCGGGAGCGAATTACAAGCGCGCACCTGAAAA

09978564.10691

FIGURE 169

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50988
><subunit 1 of 1, 560 aa, 1 stop
><MW: 58427, pI: 6.86, NX(S/T): 2
MAGPTEAETGLAEPRALCAQRGHRTYARRWVFLLAISLLNCSNATLWLSFAPVADVIAEDLV
LSMEQINWLSLVYLVVSTPFGVAAIWILDSVGLRAATILGAWLNFAGSVLRMVPCMVVGTQN
PFAFLMGGQSLCALAQSLVIFSPAKLAALWFPEHQRATANMLATMSNPLGVLVANVLSPLVLV
KKGEDIPLMLGVYITIPAGVVCLLSTICLWESVPTPPSAGAASSTSEKFLDGLKLQLMWNKA
YVILAVCLGGMIGISASFSALEQILCASGHSSGFGSLCGALFITFGILGALALGPYVDRTK
HFTEATKIGLCLFSLACVPFALVSQIQGQTLALAATCSLLGLFGFSVGPVAMELAVECSFPV
GEGAATGMIFVLGQAEGLILMLAMTALTVRSEPSLSTCQQGEDPLDWTVSLLLMAGLCTFF
SCILAVFFHTPYRRLQAESGEPPSTRNAVGGADSGPGVDRGGAGRAGVLGPSTATPECTARG
ASLEDPRGPGSPHPACHRATPRAQGPAAATDAPSRPGRLAGRVQASRFIDPAGSHSSFSSPFWVIT

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 61-79, 98-112, 126-146, 169-182, 201-215, 248-268,
280-300, 318-337, 341-357, 375-387, 420-441

N-glycosylation site.

amino acids 40-43 and 43-46

Glycosaminoglycan attachment site.

amino acids 468-471

FIGURE 170

GTCCACATCCTGCTCAACTGGGTCAGGTCCTCTTAGACAGAGCTCTGTCCATCATTTTCTGAAGTGGACCAAC
 TAGTTTCCCCAGTAGGGGTCCTCCCTGGCAATTCTTGATCGGGCTTTGGACATCTCAGATCGCTTCCAATGAGA
 TGGCTTGGCTTGGGGTCTTGCTTTGTTTCATAATCATCTAACTATGGGACAAGGTTGTGCGCGAGCTCTGGGG
 AAGGAGCAGGGGCTGATCAGGCAATCCAGGAAACACTGGAGGACTTGTTCAGGCTTTGAAGAACTCTAGTGGTT
 TCTGAATCTAGCCCACTTGGCGGTAAAGCATGATGCACTTCTGCACTTCTGTGCGGCTTTTGGGCGAGGTGG
 CTACTATTCTTTTAGGGAGATTGTGAGGAGGTGACCACTCTCAGGTTGAAATACCAAGTGTGACAGGAAGTGC
 ATCTGTGACATGATCGGGAAGCTCTCCAGGAATCTGGGCGGAGGAGAGGCGAGGCAAGCTTGGGCGCGCTT
 CCAGGTTTTCAGCTGCCCTCAGGCGCTCCCATTTCAGGTGAGCTCTGAGGAGAGGCTGTCTCAGCACAGGCGAGG
 GCTGGATCGAGAGAGCTGTGGCAGCATGGGATCCCTGCTGGTTTCTTGATGTGCTTGGCCACAGGGGATTT
 GGCCTGTGATCCATGTGGAGATCCAAGTGTGGAATCGAATGACCAACAGGCAAGGTTTCCCAAAGGCGAGCAGGA
 GCTGGAAATCTCTGAGAGGCGCTCTCTCGGAACCCGGATCCCTTGACAGAGCTCTTGACCCAGACAGGCTCC
 TAAACCCCTGACACACTCACTCTGTCTCCAGTGAGCACTTTGCCCTTGGATGTCAATTGTGGGCGCTGATGAGAC
 CAACATGCGAGAACTCATAGTGGTGAAGGAGCTGGACAGGGAATCCATTCAATTTTTGATCTGGTGTAACTGC
 CTATGACAAATGGGAACCCCCCAAGTCAGGTAACAGCTTTGGTCAAGGTCAACGTCTTGGATCCAATGACAAATAG
 CCTGGCTTTTGTCTGAGAGTTCACTGGCACTGGAATCCAAGAAGATGCTGCACCTGGTACCGCTCTCATAAAAT
 GACCGCCACAGACCTGACCAAGGCCCAATGGGAGGTGGAGTTCTTCTCAGTAAGCACATGTCCCTCAGAGT
 GCTGGACACCTTCAGTATTGATGACCAAGACAGGCGAGGTCAATTCGTGCTGACCTTAGACTATGAAAGAAACCC
 TGGCTCAGAGGTGATGATTTGAGGCAAGGGACTTGGGTCCTCAATCTATCCAGCAAGATGCAAAAGTTCTCATAA
 GTTCTTGGATGTCAATGACAACTCCAAGTCAACGTACATGGGCTCCAGCCATCTGCTGGTGTGAGAGG
 TCTTCCAAGGACAGTTTATTTGCTTGTCTGATGCGAGATGATCTGGATCAGGACACAATGGTTTGGTGTCACTG
 CTGGCTGAGCAAGAGCTGGGCACTTCAGGCTGAAAGAAGTAATGGCAACATACATATTTGGTCAACAAATGC
 CACACTGGAACAGAGCAGTGGGCCAAATATACCTCACTCTGTAGCCCAAGAACCAAGGATCTCCAGCCTTATC
 AGCCAGAGAAAGCTCAGACTCAGACTCAGTACATGACATCAAGCAATGACCTGTGGTGTGGAAGAAAGCAGGTATGA
 AGTCTCCAGCGGGGAAACAACTTACCCTCTCTCACTCATTAACCTCAAGGCTCATGATGACAGACTTGGGCTAT
 TAATGAAAGTCTCATACCGCATCAGGACTCCCAGTTGCTCACTTAGTACTAGTACTCAACACAGGAGA
 GGTCACTGCTCAGAGGTCCTGAACTATGAAGAGATGGCGGGCTTGAGTTCCAGTGTATGCGCAGGACAGCGG
 GCAACCATGCTTGATTCATCTCTGTGTGGGTGACGCTCTTGGATGCGAATGATAATGATGCGCCAGAGGTGGT
 CCAGCTGTGCTCAGGATGGAAGAAGCAGGCTCTCTGCTGCTTGTGAATGCTTCCAGAGGCAAGCTCTGTGGTGC
 CATCGAGACTCCCAATGGCTTGGGCGCAGCGGCACTGACACACCTCCACTTGGCCTACACAGCTCCCGGCCATT
 CCTTTTGACAACTATTGTGGCAGAGATGCGACTCGGGGCAAAATGGAGAGGCCCTCTACAGCATCCGCAATAG
 AATGAAGCGCACTCTTCTCACTCAACCTCATACGGGCAAGTGGAGAGGCCCTCTACAGCATCCGCAATAG
 CATTTGGAGTGTGATGGGAGCTGGAGATAGTATGAGGACAGGGGAAGCCCCCTTACAGCCCGAGGCGCTGTT
 GAGGCTCATGTTGTTGACACAGTGTGGACCACTGAGGAGCTCAGCGGCAAGCTTGGGGCTTGGAGCATGTGAT
 GCTGACGTTGATCTGCTGGCTGTATGTTTGGCATCTTCTGGGTTGATCTCTGGCTTTGTTCAATGCTCATCTGCGG
 GACGAAAGAAGACACACAGGGCTCAACTGTGCGGAGGCGAGTCCACCTACCGCAGCAGGCCAAGAGGCC
 CCGAAGAACACATCTCAAGAGGCAGACATCCACTCTGTGCTGTGCTCAGGGGTGAGCAGGTGAGCTTGTGAAGT
 CGGCGAGTCCCAAGAAAGTGTGGAAGAGGCGATGATGGAAGCAGGCTGGGAGCCCTGCTGAGGCGCCCCCT
 CCACCTCCACCCGACCTTTACAGGAGCTGCGTAATCAGGCAACAGGAGCAACCGGCGAGGACCGAGAGGT
 GCTGCAGACACAGCTCAACTCTTTTCAACCATCCAGGACAGAGGAATGCCCTCCGAGGAGAACCTGAACCTTCC
 CGAGCCCCAGCTCTGACAGGCGAGCCAGCTTCCAGGCTCTGAAGGTTGACAGGCCCCACAGGAGGCTGG
 TGGAGACAGGAGCTGAGGAAGCCCCACAGAGGCCACAGGCTCTCTGCAACCTTGAGACGGCAGCACTCT
 CAATGGCAAGGTGTCCCTTGAGAAAGAAATCAGGGCCCCGTGAGATCTCTGCGAGGCTGGTCTGTGGT
 TGGCTTCTGCGCGAGGCAAGCCCCGTGAGGAGCTCACTGTGGATCTCTCTCTGTTTCAAGAAATCTCCAGCTGCT
 GTCTTCTGTCATCAGAGGCCAATTCAGGCCAAACCAACACCGAGGAAATGAAGTCTTGGCAGGACAGGAGG
 CAGCAGGAGTGCATCCGACACAGATGGCCAAAGTGCAGGGCTGGAGGCGAGACAGCCAGAAACAGGAGGA
 AGGGCTTTTGGATGCTGGAAGAGGACCTCTCTGTGAAGCACTCTGAGAAGAGAGCTGTCAAGTCTGTCTGGAACC
 CAGCAGAGGTCTGGCCCTGGACCGGCTGAGGCGCCCTGACCGGCTGGATGGCGAGACTCTTTTGGCCCTCAC
 CACCAACTACCGTGAACATGTGATCTTCCCGGATGTGACGCCAGGAGGAGGCTTCCAGAGCTTGGG
 CAGGCGCAGGACACAGAGCTGAGGCCAACAGGCAAGGAGGCTGGCAGCAGCTTTGCTCTGGAGATGAGCTCACT
 GCTGGAGATGCTGCTGGAAAGCGCTCCAGCATGCCCTGGAGGCGCTCCGAGGCGCTCGGCGGCTCTCGGT
 CTGCGGAGGAGCCCTCAGTTTAGATCTTGGCCACAGTGCAGCCTCAGGCAATGAAGTGCAGGAGGAGCCAGGTGG
 AAGAGCGGGGATGAGGCGCAAGAGCAGGAGCAGCAGCAGCAGGAGGCTGCTGAGACATCTCAGACGCTTGC
 CTGGATCCAGAAACAGGGGCTCAGGATCTGTGGACAGAGCTGGTTCTTAAATCTTGTAACTCACTAGCTAG
 CGGCGCTCAGAACTTTTAGGTGCTGTAGTGTACCCCAACAGAGGAGCAGGAGCCCAAGCTCAACGCTGAC
 TGACCAAGAGAGCCCTTGTAGAGCAGCTCTGAGTCTTTTGGAGGACAGGAGCGTGTGTGGCTGAGATTAAGTGT
 TCTCTGGAACCATATGTGGGACACAAAGGTCAGTCTCTGCGCAACAGATGCGACGATCTACAGGAGG
 AAGGGTGGCTTCTTGGGTAGCAGGAGTCAGGGGCTGTACCTCGGGGTGCCAGGAATGCTCTTCACTTAT
 CAATAAGAGGAAAGCAGTAAAAA

09978564 10101

FIGURE 171

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48331
<subunit 1 of 1, 1184 aa, 1 stop
<MW: 129022, pI: 5.20, NX(S/T): 5
MMQLLQLLLGLLPGGYLFLLGDCQEVTTLTVKYQVSEEVPSGTVIGKLSQELGREERRRQA
GAAFQVLQLPQALPIQVDSEEGLLSTGRRLDREQLCRQWDFCLVSFDVLATGDLALIHVEIQ
VLDINDHQPRFPKGEQELEISESASLRTRIPLDRALDPDTGPNTLHTYTLSPSEHFALDVI
GPDETKHAEILIVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSDNNSPFAESS
LALEIQEDAAPGTLIIKLATDPDQGPNGEVEFFLSKHPPEVLDTFSIDAKTGQVILRRPL
DYEKNPAYEVDVQARDLGNPIPAHCKVLIKVLVDVNDNIPSIHVTWASQPSLVSEALPKDSF
IALVMADDLDSGHNGLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLTLLAQD
QGLQPLSAKKQLSIQISDINDNAPVFEKSRYEVSTRENNLPSLHLITIKAHADLGINGKVS
YRIQDSPVAHLVAIDSNTEGVTQAQSLNRYEMAGFEFQVIAEDSGQPMPLASSVSVMVSLDDA
NDNAPEVVQPVLSDGKASLVLVNASTGHLLVPIETPNGLGPAGTDTPLPLATHSSRPFLLTT
IVARDADSGANGEPLYSIRNGNEAHLFIILNPHTGQLFVNVTNASSLIGSEWELEIVVEDQGS
PPLQTRALLRVMPVTSVDHLRDSARKPGALSMSMLTVICLAVLLGIFGLILALFMSICRTEK
KDNRAYNCREAESTYRQPKRPQKHIIQADIHLVPVLRGQAGEPCEVQGSHKDVDEKAMMEA
GWDPCLOQAPFHLTPTLYRTLNRNQGNQGAPAESREVLQDVTNLLFNHPRQRNASRENLNLEP
QPATGQPRSRPLKVAGSPTGRLAGDQGSSEAPQRPASSATLRRQRHLNGKVSPEKESGPRQ
ILRSLVRLSVAFAERNPVEELTVDSPPVQQISQLLSLLHQGFQPKPNHRGNKYLAKEGGS
RSAIPDTDGSPARAGGQTDPEQEGLDPEEDLSVKQLLEEELSSLLDPSTGLALDRLSAPD
PAWMARLSLPLTTNYRDNVISPDAAATEEPRTFTQTFGKAEAPELSPTGTRLASTFVSEMSSL
LEMLLEQRSSMPVEAASEALRRLSVCGRTLSDLATSAAAGMKVQGDGPGKGTGTEGKSRGSS
SSSRCL

Important features:

Signal peptide:

amino acids 1-13

Transmembrane domain:

amino acids 719-739

N-glycosylation site.

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

Cadherins extracellular repeated domain signature.

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

FIGURE 172

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGAGTCCCGGCTGCAGCACCTGGGAGAAGG
CAGACCGTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAG
GCAGGAGCCTTCCTTACACTTCGCCATGAGTTTCTCATCGACTCCAGCATCATGATTACCT
CCCGATACTATTTTTTGGATTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTAT
GAGATACGTGATATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCAITTTTCTTGCACTAT
GTTTGAGCTCATCATCTTTGAAATCTTAGAGTATTGAATAGCAGCTCCCGTTATTTTCACT
GGAAATGAACCTGTGTGAATTCGTGTATCCTGGTTTTTCATGTTGCCTTTTTTACATTGGC
TATTTTATTGTGAGCAATATCCGACTACTGCATAAAACAACGACTGCTTTTTTCTGTCTCTT
ATGGCTGACCTTTATGTATTTCTCTGGAACCTAGGAGATCCCTTTCCCATTTCTCAGCCCAA
AACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTTGGTGTGATTGGAGTGACTCTC
ATGGCTCTTCTTCTGGATTGGTGCTGTCAACTGCCCATACACTTACATGTCTTACTTCTCT
CAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAAACCATGGATA
TGATCATAAGCAAAAAGAAAAGGATGGCAATGGCAGGAGAACAAATGTTCCAGAAGGGGGAA
GTGCATAACAAACCATCAGGTTTCTGGGGAATGATAAAAAGTGTTACCCTTACAGCATCAGG
AAGTGAATACTTACTCTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGC
TTTTTCTGGAACAGCTGATCTATATGCTACCAAGGAGAGAAATAGAATACTCCAAAACCTTC
AAGGGGAAATATTTTAATTTTCTTGTTACTTTTTTCTCTATTACTGTGTTTGGAAAATTTT
CATGGCTACCATCAATATTGTTTTGATCGAGTTGGGAAAACGGATCTGTCAAGAGGCA
TTGAGATCACTGTGAATTATCTGGGAATCCAATTGATGTGAAGTTTGGTCCCAACACATT
TCCTTCATTCTGTTGGAATAATCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTAC
CAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCTCCAATGTCAATTGTCTGTCTATTAGCAC
AGATAATGGGCATGTACTTTGTCTCCTCTGTGTCTGCTGATCCGAATGAGTATGCCCTTAGAA
TACCGCACCATAACTACTGAAGTCTTGGAGAACTGCAGTTCAACTTCTATCACCGTTGGTT
TGATGTGATCTTCTGTGTGAGCGCTCTCTAGCATACTCTTCTCTATTGAGCTCACAAC
AGGCACAGAGAAGCAAAATGGCACCTTGAACCTAAGCCTACTACAGACTGTTAGAGGCCAGT
GGTTTCAAATTTAGATATAAGAGGGGGGAAAAATGGAACCAGGGCCTGACATTTTATAAAC
AAACAAAATGCTATGGTAGCATTTTTTACCTTCATAGCATACTCTTCCCGTCAGGTGATA
CTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGAGAACTAACTCAAGACAAATACTCA
GCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGAGAGGAGCCAAAGAACTAA
AGGTGAAAAATACACTGGAACCTCTGGGGCAAGACATGTCTATGTTAGCTGAGCCAAACAGT
AGGATTTCCGTTTAAAGTTTACATGGAAGGTTATAGCTTTGCCTTGAGATTGACTCATTT
AAAATCAGAGACTGTAACAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCG
ACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTTTATGTCAGCTTATAATG

10076564.10501

FIGURE 173

MSFLIDSSIMITSQILFFGFGWLFFMRQLPKDYEIRQYVVQVIFSVTFAPFSCTMFELIIFEI
LGVLNSSSRYPHWMNLCVILLILVFMVPPYIGYFIVSNIRLLHKQRLLFSCLLWLTFFMYFF
WKLGDPPILSPKHGILSIEQLISRVGIVGVTLMALLSGFGAVNCPYTYMSYFLRNVTDDI
LALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQ
QEVDALEELSRLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVF
DRVGKTDPPVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFYFAISS
SKSSNVIVLLLAQIMGYFVSSVLLIRMSMPLEYRTTIITEVLGELQFNFYHRWFDVIFLVSA
LSSILFLYLAHKQAPEKQMAP

Important features:

Signal peptide:

amino acids 1-23

Potential transmembrane domains:

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,
425-444

N-glycosylation sites.

amino acids 67-70, 180-183 and 243-246

Eukaryotic cobalamin-binding proteins

amino acids 151-160

0078564.301001

FIGURE 174

CATGGGAAGTGGAGCCGGAGCCTTCCTTACACTCGCCATGAGTTTCCTCATCGACTCCAGCA
TCATGATTACCTCCCGANACTATTTTTTGGATTGGGTGGCTTTCTTCNGCGCCAATGTT
TAAAGACTATGAGATACGTCAGTATGTTGTACNGGTGATCTTCTCCGTGACGTTTGCCATTT
CTTGCACCATGTTTGAGCTCATCATCTTTGAAATCTTNGGAGTATTGAATAGCAGCTCCCGT
TATTTTCACTGGAAATGAACCTGTGTGTAATCTGCTGATCCTGGTTNTCATGGTGCCCTTT
TTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTT
CCTGTCTCTTATGGCTGACCTTTATGTATTTCCAG

0997564.101601

FIGURE 175

GTGTTGCCCTTGGGGAGGGGAAGGGGAGCCNGGCCCTTTCCCTAAAATTGGCCAAGGGTTTC
TTTNTTGAATTCGGGTTNNGNATACCTTCCCAGAAAATATTTTTTGGATTGGGGTAGNTT
TTTTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGGTGATNTT
NTCCGTGACGTTTGCATTTTCTTGCACCATGTTTGAGCTCATCATNTTTGAAATNTTAGGAG
TATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATCTGCTGATC
CTGGTTTTTCATGGTGCCTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCA
TAAACAACGACTGCTTTTTTCCTGTCTNTTATGGCTGACCTTTATGTATTTNTTNTGGAAAN
TAGGAGATCCCTTTCCCATTCTC

09978554.101501

2003/04/24 15:07

TGCTGGCAGGGATCTGTCCTCATGCGCCGGGGCTCGGAGCCGCAACCTTTGGGGGGCCCTCGGGAAATTGCTCACTTTT
TGCGCTCTCTGCTCTGCAAGTCTTCTCTCTACCGAGGCTGTGCGCTCTCAATCTGAGCGATGATGGGTGCTCTTGCGCAAA
GGAGGGCGGAGCGAGGCAAGCTCTTGCGGCTTCTTGCGCTCTGACCGGATGTGACGGAGCCAGCCAGAGCTGCTG
CTCTGCTGGTGGTGGTCTCCCGCAGAGCTCTGGCTCTCTTGCGGGCAGCAGCGACATCGCATGTGAGAGCGTTTGCTGCTGT
CCCGTGTGAGCTGTGGAGGAATCTGA CTGCTACAGATGTGA CATCGACAGGAGATGATATGTGAAAAAGCAAGCAAA
GGAGAAACCAAGTGTGGAGATCTAGTGTCTCGAGCGAGGGGCTGGGGGGCAAGATTTGTACTCTGTGCACACCGATAT
TAGAGCAAGAGCAGGAGTGAACAAGATCTGGAGAGCGGGGATATGATTGCTGTCTGCTTTTGGTCTCGACCGAGGA
CTCGGCCATCTCGGGATAGATTGAGTGGTGGGGAATGGAGATTTCTGTGAGGAGGAGCCGCCCAAGCGCATGAACAAAT
TTGGGTTTCTCGACAGGCGACAGTCTGCGTCCGCCCTCTCTCCCTGATGACATCTACCTCTCTTTGGGGCCGAGGAAT
CTATAATTGTGAAGAGGCGAGCGCAGAGGTGGAGCTCTGTGACAGGGCTCAGCGGACATGGGCACATCTGAGCAACGCT
TCCCTACAGGGCGGGGGAGAGAGGAGCAGGACCGCCGCCCTCTCCCGCTGCTGCCACAGCTACTTTGGCTTT
TCTTATTGATCTCGGGGAAAGGCTTGGTGGTCTGTGCTGTGCGAAGAGAGAGTCTTGTGGTGGAGGCCCCCGCGGCCAACCA
CAAGGGTGTGTGGTGTCACTTCTGCGCAAGGACAGCGCAGTGCCTGTGTGCCGAGGTATTGCTGTCTGGGAGAGG
CTCGAATCTCCGGCTTTGGCTACTACTTGGCTTGGCTGACCTCAACAGTAGTGGCTGGCCAGACTGTCTGGGAGAGG
TGCCCCCTACTTTTGTGAGCGCAAGAGAGCTGGGGGTGCTGTGTATGTGACTTGTGAACAGGGGGGTTCACTG
GGCTGGGATCTCCCTCTCTCGGCTCTGGCGCTCCCGTCACTCCATCTGCTGGGATGTGATGGAAAGTCTTCACTTACCA
CTCAACCAAGATGGCTTTCCAGATATTCAGTGGGTGCCCTTTGATGTGTGATGGAAAGTCTTCACTTACCA
TGGGAGGAGCTTGGGGGTTGTCCGCAAACTTTCAAGGTGTGAGAGGGGAGGCTGTGGGATCAAGAGATCTCTGG
CTACTCCCTGTGACGAGCTTGTGATAATGGATGGGGAAACCAATCCCTGACCTGGTGTGGGTGCCCTCTGGCTGACAC
CGAGTGTCTTTACGGCGCAGAGCCCATCTCCATGTTCTCCATGAGTGTCTATTGTCTCCAGAAGATCGACT
GGAGCGGCCCAACTGCTGCTGGCGGCACCTCGTCTGTGTGTGAGCACTAAGGGTCTGTTTGTGAGTACATTCGATCT
CAGCAGCTATAGCCCTACTGTGGCTCGGATCTGTGTGTGATGTCCGGAACAGACAGGAGGCTCGGGGCAAGCTGTGG
TCCCGTGTGACAGTCTCTGAGCGCTAATCTGGAGAAACCAAGCAGCAGGCTCGGGCAGCGTGTGGCTGTGAAGCA
CCAGATGACAGAGTCTGTGGAGAGCGCATGTTCCAGCTGTGAGCAAGAAATGTCAAAGCAAGCTCTGGGCCATTTG
AGTGAACCTTTGCTTACAGTCTCGACAGCTCCGCTCGGCTCGGGCAGAGCAAGCTCTTGAGCCAGGGGCTGCTCTCAGTGG
CCCATCTCAATGGCCACAGCCAGCAGCAGCCAGGGGAGAGATCCATCTTGAAGCAAGGCTGTGGTGTGAAGA
CAAGATCTGGCAGAGCACTCTCAGCTGTGTCAAGCTGCTGTATCCAGTGTTCAGCAGAGCAAGAAATCTCAACT
TGTGCCCATGTGATGTGATGGAAACAGACCGCTTTTGCTCATGATGGGCGAGCATTTGGCTGGAGTCTAGT
GGTCAACCAAGCTGCCATCGACAGCCAGGCCAGCCGAGCATGTGGGATGTGTCCTATGAAGCCAGCTCTGTGT
CATGCTCTTGACTCATCTGACTACTCAGGAGTCTGGGGCGCTGAGACCTGTGGAGAAAGCCATCTGCTGTCTCAA
TGAAGATGCTCCCATGTGTGATGTGAGTGGGAAACCCATGAAGAGAGAGTGGCCAGTCACTTTCTATCTCAT
CTTGAGCTCTCCGGATCAGATTTAGACACAGCAATCGAGTGTGAGTGTGAGTCTGTTTGGCCAGCATCTAGTAGACA
GGAGCTGACTTCCAGTCTCTGACAGAGCGGCTGTCTTATGTAGCTGAGCTGACCTGATTCAGGAATGGCCATCTCC
CCAGCAATCTTCTTCTCTGTGTGGTGGAGGCGAGAGACATGACATGTGAGCGGATGTGGGCAAGCAAGT
CAAGTATAGGTTGACGGTTTCTCAACCAAGGCCAGCTGCTCGAAGAACCTGGGCTCTGCCCTTCTCAACATGATGTG
CGCTCATGAGATGTCCAAATGGGAAGTGTGTCTGTACCAATCAGGTTGATGCTGAGGGCGGGCAGGGCTCTGG
GCGAAGAGGGCTTTGTCTCTCCAGGCCCAACATCTCCACCTGGATGTGGACAGTAGGGATAGAGGCGCGCGGGA
GCTGGAGCCACTGAGCAGCAGGAGCGTGTGTAGCGGCGAGGACCCAGCATGTCTGTGTGGGAGTGGGCGCGGGA
TGAGAAAGAGAAAAACATCCCTGGATCGCGCCCGGGCAGCGGCACATGTCTGTGTGGGCGAGTCTCTGTGGT
CAGCTTTGACCGCGCGCTGTGCTGATGTTCTGGGCGGCTCTGGAAACAGCACTTTCTGGAGAGGATCTCAGCT
TGTGAAGCTCTGGAAGTGAATGTGTCGAGGCCAACATCATCAAGCTGAAGTCTCTTCCGGAAGA CCGACAGCA
TGGCTCCAGCTGTCTCCAGTGAATGTGATATCTATGGAACCTGAGTGTGAGTCTCTTGAAGATGGGAATCTT
CATCTCTCTGCTGTACTGTGCTGGGCTGTCTGTGTGTAGCACTGTGTGTGTCTGTCTTGTGTGAAGATGGGAATCTT
CAAA CGGGCAGGACCCCGAGGCCACCTGTGAGGAAACATGTGGGCGAGCCCGCGGGAGGGCCGGATGTGACA
GTTCAAGAGAGAGAAGAGCGGCACCTCTGAGGAAACATGTGGGCGAGCCCGCGGGAGGGCCGGATGTGACA
CCCATCTCTGCTGTCTGACCGGCATCCGAGTCTGGGCCCGGATGGGCATCTCAGGGCCGAGCCAGCTAGGTTCTC
CATGCTCCAGCTTGGCTGTGGTGTGCCCTCTCATCTCTCCAGAGATGGTCTCTTGGGATGAGAGGTTAGAT
GGGCTGGCTGTGTGCTGATCAAGATTTGGCAGATGTGCTCTCTCAGGGCCAGCAGACTCTCCACCAACAAGAC
TCTCCCGCCAGCTTCTTCCCTTGAGAGTGTGTGATGATGAGATGGGTAAATCAGGCAAGGGCCAGTGGGTGAGG
TGAGAAGAGCGAGGGTGTCTGATGTCAAGAGTGGGGAGAGGAGATCTTAATCTCTTCTCTCATCTACCTGT
GTAAAGCAGGACCAAGGAACCTGCTCTCCCGGAAGTGTCTTAATCTAGAGGCTGGGGAGAGGTTGTGTCTCATGTA
CTGCGTGTCTCTCTCTCTAGTTTCCCTCTCATCTGACCTTAGTTTGTGTCGCTCAGTCTAGTGTGTTTCTGTGGT
TCTGCTCTATTATTAAAAAATATTGTAGAACAAAAAATAAAAAAATAA

FIGURE 177

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737

>subunit 1 of 1, 1141 aa, 1 stop

><MW: 124671, pI: 5.82, NX(S/T): 5

MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQL
QPRPQSWLLVGAPQALALPGQQAARTGGFLFACPLSLEETDCYRVDIDQGADMQKESKENQWL
GVSVRSQGGPGGKIIVTCAHRYEARQVRDQILETRDMIGRCFVLSQDLAIRDELDDGGGEWKFC
RPGQHEQGFQCQOQGTAAAFSPDSHYLLFGAPGTYNWKGATARVELCAQGSADLAHLDDGPYEA
GGEKEQDPRILIIPVANSYFGFSIDSGKGLVRAEELS FVAGAPRANHKGAVVILRKDSASRLV
PEVMLSGGERLTSGFGYSLAVADLNSDGDWPD L I V G A P Y F F E R Q E E L G G A V Y V Y L N Q G G H W A G I
SPLRLCGSPDSMFGISLAVLGDNLQDGFDPDIAVGAPFDGDGKVFIYHSSSLGVVAKPSQVLE
GEAVGIKSPFGYSLSGSLDMDGNQYPDLLVGLADTAVLFRARPILHVSHEVSIAPRSIDLEQ
PNCAGGHSVCVDLRVCFSYIAVPSSYSPTVALDYVLDAITDRRLRGQVPRVTFLSRNLEEPK
HQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSSYSLQTPRLRRQAPGQGLPPVAP
ILNAHQPSQRAEIHFLKQCGGEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVDGTTALFA
LSGQPVIGLELMVTNLPSDPAQPPQADGDDAHEAQLLVMLPDSLHYSGVRALDPAEKPLCLSN
ENASHVECELGPNMKRGAQVTFFYLILSTSGIS IETTELEVELLATISEQELHPVSARARVF
IELPLSIAGMAIPQQLFFSGVVRGERAMQSERDVGSKVKYEVTVSNQGSRLTIGSAFLNIM
WPHEIANGKWLLYPMQVELEGQGPGQKGLCSRPNNILHLDVDSDRRRRRELEPEQPEGE
RQEPSMSWWPVSSAEKKKNITLDCARGTANCVVFSCLPSYFDRAAVLHVWGRLLWNSTFLEEY
SAVKSLEIVVRANITVKSSIKNLMRLDASTVIPVMVYLDPMVAVAEVGPWWVILLAVLAGLL
VLALLVLLWKMGFFKRAKHPEATVPQYHAVKIPREDRQQFKEEKTGTILRNNWGSFRREGP
DAHPIAADGHPGLGDGHPGPGTA

Important features:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 1040-1062

N-glycosylation sites.

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

Integrins alpha chain proteins.

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

FIGURE 178

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGCGGTGCAGCAGCTCCAGA
AAGCAGCGAGTTGGCAGAGCAGGGCTGCATTTCAGCAGGAGCTGCGAGCACAGTGTGGCT
CACAAACAAGATAGCTCAAGGTGTGAGCCGTACTGTGTGTGTGTGCAGCCGCTTGGTGCAGTCA
GTCTCTCGCAGCTGCCGCGGCGGTGGCTGCAGCCGGGGGCGGTGCGACGGCGGTAATTTTC
TGGATGATAAACAAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGGACAGTGGAAC
AAATTCGAGACGAAGTAGAGGATGATTATTTCCGCACTTGGAGTCCAGGAAAACCCCTCGA
TCAGGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTGCCTATAAGTAT
GCATTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATG
AAAGAAGCAGGAGTAGACCATAGGCAGTGGAGGGGTCCCATATTATCCACCTGCAAGCAGTG
CCCAGTGGTCTATCCAGCCCTGTTTGTGGTTCAGATGGTCATACCTACTCTTTTCAGTGCAC
AACTAGAATATCAGGCATGTGTCTTAGGAAAAACAGATCTCAGTCAAATGTGAAGGACATTGC
CCATGTCTTTCAGATAAGCCCAACAGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGCACCT
GGAGTTCAGGGAAGTGGCAACAGATTGCGGGACTGGTTCAGGCCCTTCATGAAAGTGGAA
GTCAAAAACAAGAAGACAAAAACATTGCTGAGGCCCTGAGAGAAGCAGATTGCATACCAGCATC
TTGCCAATTTGCAAGGACTCACTTGGCTGGATGTTTAAACAGACTTGATACAACTATGACCT
GCTATTGGACCACTCAGAGCTCAGAAGCATTACCTTGATAAGAATGAACAGTGTACCAAGG
CATTCTTCAATTCTTGTGACACATACAAGGACAGTTTAATATCTAATAATGAGTGGTGCTAC
TGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTCAGAAGCGGCA
AGGGGTAAAGAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGC
CAACACAATGTCTATGGCAGTGTGGACAGTGTGGTGTGTGACAGATATGGAATGAAGTC
ATGGGATCCAGAATAAATGGTGTGTCAGATTGTGCTATAGATTTTGAGATCTCCGGAGATTT
TGCTAGTGCGGATTTTCATGAATGGAAGTGTGATGAGGATGATGAAGACGATATTATGAATG
ATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTGTGAC
CATGATGTATACATTTGATTGATGACAGTTGAAATCAATAAAATTCTACATTTCTAATATTTA
CAAAAATGATAGCCTATTTAAAATTATCTTCTCCCAATAACAAAATGATTCTAAACCTCA
CATATATTTGTATAATTATTTGAAAAATTGCAGCTAAAGTTATAGAACTTTATGTTTAAAT
AAGAATCATTTGCTTTGAGTTTTTATATTCCTTACACAAAAAGAAAAATACATATGCAGTCTA
GTCAGACAAAAATAAGTTTTGAAGTGCTACTATAATAAATTTTTACAGAGAACAAACTTTGT
AAATCTTCCATAAGCAAAATGACAGCTAGTGTCTGGGATCGTACATGTTAATTTTTTTGAAAG
ATAATCTAAGTGAAATTTAAAATAAATAAATTTTTAATGACCTGGGTCTTAAGGATTTAGG
AAAAATATGCATGCTTTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAG
GATAACAGAGAGATACCACATGACTCCAAAAAAAAAAAAAAAAA

FIGURE 179

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49829
><subunit 1 of 1, 436 aa, 1 stop
><MW: 49429, pI: 4.80, NX(S/T): 0
MLKVSAVLCVCAAAWCSQSLAAAAVAAAGGRSDGGNFLDDKQWLTTISQYDKVEVGQWNKFR
DEVEDDYFRTWSPGKPFQALDPAKDPCLMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEA
GVDHRQWRGPILSTCKQCPVVYPSFVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCP
SDKPTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSQNKTKTLRPERSRFDTSILPI
CKDSLGMFMNRLDTNYDLLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNNEWCYCFQ
RQQDPPCQTELSNIQKRQGVKKLLGQYIPLCEDDGYKYPTQCHGSGVQCWCVDRYGNEVMGS
RINGVADCAIDFEISGDFASGDFHEWTDDEDEDDIMNDEDEIEDDDEDEGDDDDGGDDHVDYI

Important features:

Signal peptide:

amino acids 1-16

Leucine zipper pattern.

amino acids 246-267

N-myristoylation sites.

amino acids 357-362, 371-376 and 376-381

Thyroglobulin type-1 repeat proteins

amino acids 353-365 and 339-352

0070564 101601
109121 1092760

FIGURE 180

CAGACTCCAGATTTCCCTGTCAACCAAGAGGAGTCCAGAGAGGAAACGCGGAGCGGAGACAACACAGTACCTGACGC
 CTCTTTCAGCCCGGGATCGCCCGCAGGAGATGGCGCACAAGATCTGCGTCCCTTCCCGCTGCTCTCTTGCCCT
 GCTCTGCCCTCGGCTGCTGCTGCTGGGGCGCGCGGCTTCCACCTTCCCTCGATAGCGACTTCACTTTTACCTCT
 CCGCGCGCGCAGAAGGAGTCTCTACAGCCCATGCCCCCTGAAGGCCCTCGCTGGAGATCGAGTACCAAGTTTAA
 GATGGAGCAGGATTAGATATTGATTTCCATCTTGCCCTTCCAGAAAGGCAAAACCTTTAGTTTGTGAACAAAGAAA
 TCAGATGGAGTCTGATCTGACAGCTGAAGTCTGGTGTATTCATGTTCTGCTTTGACAAATACATTTCAGCACCATT
 TCTGATAGAGGTGATTTCTTTGAATTAATCTCGGATAATATGGGAGAACAGGCACAAGAACAGAGATTGGAAAG
 AAATATATTAATCTGGCACAATATATTGGATATGAACCTGGAAGACATCTGGAAATCCATCAACAGCATCAAGTCC
 AGACTAAGCAAAAGTGGGCACATACAAAATTCGCTTAGAGCATTTGAAGCTCTGATCGAAACATACAGAAAGC
 AACTTTGATAGAGTCAATTTCTGGTCTATGTTTAATTTAGTGGTCTATGGTGGTGGTGTCAAGCATTCAAGTTTAT
 ATGCTGAAGAGTCTGTTTGAAGATAAGAGGAAAGTAGAACTTAAACTCCAACTAGAGTACGTAACATTGAAA
 AATGAGGCATAAAAAATGCAATAAATCTGTACAGTCAAGACCATTAAATGGTCTTCTCCAAAATATTTCAGATATA
 AAAGTAGGAACACAGGTATAATTTTAAATGTGAAAAATTAAGTCTTCACTTCTGTGCAAGTAACTCTGCTGATCCAG
 TTGTACTTAAGTGTGTAAACAGGAATATTTTGCAAGATATAGGTTTAACTGAAATGAAGCCATATTAAATACTGCAT
 TTCTTCACTTTGAAAAATTTTGCAAATGTCTTAGGTGATTTAAATAATGAGTATTGGGCCATAATTGCAACACC
 AGCTGTTTAAACAGGTTCTATTACCCAGAAGCTTTTGTAAATGCGGCAGTTCAAAATTAACGTGGAGGTTT
 TCAGTTTAAAGTTATAAATCACTGAGAAATACCTAATGATGGATTGAATAACTTTAGACTATAGTATAGGATGAAA
 CTCTTTCTCTATTACATATGCAATCTCTCTATAATGTAATAGAATAATAGCTTTGAAATACAAATTTAGGTTTGTG
 AGATTTTATAACCAAAATCACTTTCAGTGAACATATTAGCAGAAAGCATTAGCTTTTGTACTTTGCTTTACATCT
 CCAAAGCTGACATTTTACAGATTCTTAAACACAAAGTTTACCTTACTTAAATATAGGACATGTTTCTCTTTG
 AAATGAAGAAATATAGTTTAAAGCTTCTCTCCATAGGGACACATTTCTCTAACCTTAACTAAAGGTGAGGA
 TTTTAAATTAATGTGAGGTAAATAAGTTTATTTTAAATAGTATCTGTCAAGTTAATATCTGTCAACAGTTTAA
 TAATCATGTTTATGTTAAATTTAAACATGATGCTGACTTGGATAATCTTAACTAACCGAGTTGTCAAGGAAATA
 TTGCTAAATGATCTGGGCCATACCATAAATAAATCTCTCTTCTGAGCTCTAAGAAATCTCAGAAACAGGAA
 AGAATTTAGAAAACTTGAGAAACCTTAATCCAAATAAATACTTCTTAACTTAACTAAGATCTATGAATCTAGA
 ATCTGACTGGCTCATCATGACCTCTTCTCATAACTAAATCAAAGGAGATGATTAATTTCCAGTTAGCTGGGAAG
 AAATTTGGCTGATGTTTATTTTCTCAAGAAATCTGGTGTGAATTTTGTGAAGCAGGTACATTTTATA
 AAATGTAAGCCCTTACTGTGAAGTTTAGCACTGGGTGTACATATTATTAATAAATTTTATTAACACACTTTTAT
 TAAATTTGGCCTTTCTGAACACTTTATTTTATGATGTTGAAGTAAGGATAGAAACATAGACTCCCAAGTTTAA
 CACTTAATGTGAATAACCATATAACAACAAAGTTTCTGCACTTATGTTTGAAGTCTATGGGGTCTTAC
 TCAAGTACTAGTAATTTAACTTCTATCATGTAATGAATCTTATTTGAAGTCTATGGGGTCTTAC
 GACTACATTTGTGAGTTAGAAACAACTTAAATTTGGGGTATAGAACCCTCAACAGGTTAGTAATGCTGGAATT
 CTTAGTAGACATTAATGATTAACCAAGAGTGATTTCACTCATAGTAGTATAAAAGAGATACATTTCCC
 TCTTAGGCCCTCGGAGAGAGCAGCTTAGATTTCCCTACTGGCAAGGTTTTTAAATAGAGTAAATGCGGTAT
 ATGCAATTAATCTTAAATGGCCAGAAAATGCTTCAGGTGTCTAGGGGTATCTCTTGCAACACTTGCAGAACAA
 AGGTCAATAGAGTCTTGCTGATGAATACCCCTCCCTTTGCGCTGTAAATTTGCAATGAGAAGCAAAATTTACA
 GTACCAATAAATAAAGCAGGGTACAGATATAAATCTGTCATCTTTCTATAAACTGTGATTAAGAATTCTA
 CCTCTCTGTATGGCTTACTGTACTGTACTCTGTACTCTTACCTAACAAATGAATTTCTATACTTCTCT
 ACATGATGATTTGTGCCACTGATCTTAAACCTATGATTCAGTAATCTTACATATAAAACAGATAATTTGCTT
 TATTTGAAAAAGAAATTTAGGAATCAAGGACAAATTTTATAGACAAAGTAAGAAAGACAGATATTAAAGAGG
 CACTCAACAAAAGCAAAATCTGTAAACAGAGTAAAAATCTTTAAATTTCTTAAAGACATACCTGTTTATCTGCTT
 CATATGCTTTTAAATTTCACTATTCCATTTCTAAATTAAGATTATGCTAAATGAGTAGAGCTGTTTATCACTT
 AACAGCTCATTTTGTCTTTTCAATATACAAATTTAAAAATACTACAATAATTAACTAAGGCCAACCCGATTAT
 CATAGTGTAGAGGTTACCGTGTACCTCACTAAGGCCTAGAGTTTGTCTGATATGCAATTTGGATGATTAAT
 GTTATGCTGTTCTTCACTGTAATGTCAAGCATGGAGGGTGTGTAATTTTATGTAATAATTAATCCTTCTTA
 CACATAATGGTGTCTTAAATTTGCAAAAAATGAGCACTTACAATGTATGTTCTCTCAATGAAGATTCTTAT
 GTGAATTTTAAAGACATGATTTCGCGATGAAGGATTTTCTATCTGAAGTACAAATATGACAAATCAGTGTG
 CTCAACTGCTTTATACTTATAAACAGCCATCTTAAATAAGCAACGTATTGTGAGTACTGATATGTATATAATA
 AAATATCAAGGAAAA

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INCUBATOR = 40-45°C

```
><subunit 1 of 1, 229 aa, 1 stop
```

MGDKIWLPPFVLLAALPPVLLPGAAGFTPSLSDSFTFTLPAGQKECFYQMPMLKASLEIEY
QVLGDGAGLDIDFHLASPEGKTLVFEQRKSDGVHVTETEVGDYMFCDNTFTSTISEKVIFFEL
ILDNMGEQAQEDEDWKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDRN
IQESNFDRVNFWSMVNLVVMVVSAIQVYMLKSLFEDKRKGR

Signal peptide:

Transmembrane domain:

N-myristoylation site.

Tyrosine kinase phosphorylation site.

amino acids 55-62

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CCATCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATACCAGAT
CTCACCAGAGAGTTCGAGACACTATGCTGCCTCCCATGGCCCTGCCAGTGTGTCTCTGGATG
CTGCTTTCTGCTCATTCTCTGTGTCAAGTTCAAGGTGAAGAAACCCAGAAGGAACTGCC
CTCTCAACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGT
TTTTGTCAACAAATCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGA
CTGGTGTCTGTCTCAGTGGGGCTGAGGGATCCTTCGTGTCTCCTCGGTGAGGAGCATTAG
TAACAGCTACTCATACATCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATG
GAGATGGATGGGAGTGAGAGTAGCACTGATGTGATGAATTACTTTGTCATGGGAGAAAAATCCC
TCCACCATCTTAAACCTTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTG
GAAAGATTATAACTGTGATGCAAAGTTACCCATATGTCGCAAGTTCAAGGACTAGGGCAGGT
GGGAAGTCAGACCACTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGAC
TCACCCTGGAGAGAAATATTTCTCCCCAAATCGCCCTACCTGACTACCTTGTATGATCTCTCC
TTCTTTTTCCTTTTCTTCTACCTTCACTTTCAGGCTTTCTCTGCTCTTCCATGTCTTGAGATC
TCAGAGAATAATAATAAAAAATGTTACTTTATAAAAAA
AAAAAAAAAAAAAAAAA

FIGURE 183

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965
<subunit 1 of 1, 175 aa, 1 stop
<MW: 19330, pI: 7.25, NX(S/T): 1
MLPPMALPSVSWMLLSCLILLCQVQGEETQKELFSPRISCPKGSKAYGSPCYALFLSPKSWM
DADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSS
TDVMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLEYVCKFKD

Important features:

Signal peptide:

amino acids 1-26

C-type lectin domain signature.

amino acids 146-171

09973664-101601

FIGURE 184

CCAGTCTGTGCGCCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGAGC
ACAGAGGAGTGGGCCGGGACCATGCGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGTGGC
TGCTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCACAGGAGTGT
CGGACTGTGTCACCATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCACACTCTAC
TCCCGGGAGATAGTGTACCCCTTCCAGGGGGACTCCACGGTGACCAAGTCCTGTGCCAGCAA
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCCTGCCCGTGTCTGTGCAATACTG
AGCTGTGCAATGTAGACGGGGCGCCCGCTCTGAACAGCCTCCACTGCGGGGCCCTCACGCTC
CTCCCACTCTTGAGCCTCCGACTGTAGAGTCCCCGCCACCCCATGGCCCTATGCGGCCCA
GCCCCGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAAAAAAAAAAAAAAAA

097854-101501

FIGURE 185

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405

<subunit 1 of 1, 125 aa, 1 stop

<MW: 13115, pI: 5.90, NX(S/T): 1

MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP
FQGDSTVTKSCASKCKPSDVGIGQTLPVSCCNTEL CNVDGAPALNSLHCGALTLLPLLSLRL

Important features:

Signal peptide:

amino acids 1-17

N-glycosylation site.

amino acids 46-49

00973564-101601

FIGURE 186

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGACCTTGACTCTGCAGCCGAACCGGC
ACGGTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTTTTCTTCTCCCTCTT
GAGTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTGCGGATGG
TAGCGGCGGCTCTCGGCGGCCACCTCTGCTGGGAGTGAGCGCCACCTTGAACTCGGTTCTC
AATTCCAACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTC
TGCAGTCAGCGCCGCGCGCGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA
ACTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCAGCACTGATGAGTACTGCGCTAGT
CCCACCCGCGGAGGGGACGCGAGGCGTGCAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACG
CTGCATGCGTCACGCTATGTGCTGCCCGGGAATTACTGCAAAAATGGAATATGTGTGTCTT
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT
CATAGCACCTTGGATGGGTATTCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAA
AGGACAAGAAGGTTCTGTTTGTCTCCGGTCATCAGACTGTGCCCTCAGGATTGTGTTGTGCTA
GACACTTCTGGTCCAAGATCTGTAAACCTGTCTGAAAGAAGGTCAAGTGTGTACCAAGCTA
AGGAGAAAAGGCTCTCATGGACTAGAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTC
TTGCCGATACAGAAAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACACTTGTGAGA
GACACTAAACAGCTATCCAAATGCAGTGAACCTCTTTTATATAATAGATGCTATGAAAACC
TTTTATGACCTTCATCAACTCAATCCTAAGGATATACAAGTTCTGTGTTTTAGTTAAGCAT
TCCAATAACACCTTCCAAAAACCTGGAGTGTAAAGAGCTTGTCTTTATGAACTCCCTG
TGATTGCAGTAAATTAAGTATTGTAAATCTCAGTGTGGCACTTACCTGTAAATGCAATGA
AATTTTTAATTATTTTCTAAAGGTGCTGCACTGCCTATTTTCTCTTGTATGTAAATTT
TTGTACACATTGATTGTTATCTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCATT
TCAGCTTATAGTTCTTAAAGCATAACCTTTACCCATTAAATTTCTAGAGTCTAGAACGCA
AGGATCTCTTGAATGACAAATGATAGGTACCTAAAATGTAACATGAAAATACTAGCTTATT
TCTGAAATGACTATCTTAATGCTTAAATTAATATTCCCTTTAGGCTGTGATAGTTTTTGA
AATAAAATTTAACATTTAAAAA

0973564.101601

FIGURE 187

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57530
<subunit 1 of 1, 266 aa, 1 stop
<MW: 28672, pI: 8.85, NX(S/T): 1
MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSA
APGILYPGGNKYQTIDNYQPYPCAEDDECGTDEYCASPTRGGDAGVQICLACRKRRCMRH
AMCCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRTTLSSKMYHTKGQEG
SVCLRSSDCASGLCCARHFWSKICKPVLKEGQVCTKHRRKGSHGLEIFQRCYCGEGLSCRIQ
KDHHQASNSSRLHTCQRH

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 256-259

Fungal Zn(2)-Cys(6) binuclear cluster domain

amino acids 110-126

FIGURE 188

TGTGTTTCCCTGCAGTCAGAATTTGGGACNGCAGGGGTTCCCGGACCTGATTTTGCAGCGGA
ACGGGAAGGTTTTGTGGGACCCAGGTTGAAATGACGGTCATTTTTTTTTCTTCTCCTTCNG
GAGTCCTTNTGAGANGATGGTTTTGGGCGCAGCGGGAGCTAACCCGGTTTTTTGTNGCGATG
GTAGCGGCGGTTTTTCGGCGGCCACCTTNTGCTGGGAGTGAGCGCCACCTTGAATCGGTTTTTC
AATTCCAACGNTATCAAGAACCTGCCCCACCGNTGGGCGGCGCTGCGGGGCACCCAGGNTT
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA
ATTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT
CCCACCCCGGAGGGGANGCGGGCGTGCAAATNTGTNTNGCCTGCAGGAAGCGCCGAAAACG
CTGCATGCGTCANGCTATGTGCTGCCCGGGAATTACTGCAAAAATGGAATATGTGTGTTNTT
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT
CATAGCACCTTGGATGGG

1097364.01601

2005/06/24 14:16:16

[illegible]

FIGURE 190

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56439
<subunit 1 of 1, 747 aa, 1 stop
<MW: 86127, pI: 7.46, NX(S/T): 2
MGVWLNKDDYIRDLRKIILCFLIVMAILVGTDQDFYSLLGVSKTASSREIRQAFKKLALKL
HPDKNPNNNAHGDFLKLINRAYEVLKDEDLRKKYDKYGEKGLDNQGGQYESWNYRYDFGI
YDDDPEIITLERREFDAAVNSGELWFVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNC
GDDRMLCRMKGVNSYPSLFI FRSGMAPVKYHGD RSKE SLVSFAMQHVRS TVTELWTGNFVNS
IQTAFAAGIGWLITFCSKGGDCLTSQTRLRLSGMLF LNSLDAKEIYLEVIHNLDPDFELLSAN
TLEDRLAHHRWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICS NLYVFQP
SLAVFKGGTKYEYIHHGKKILYDILAFAKESVNSHVTTLG PQNF PANDKEPWLVDFFAPWC
PPCRALLPELRRASNLLYGLKFGTLDCTVHEGLCNMYNIQAYPTTVVFNQSN IHEYEGHHS
AEQILEFIEDLMNPVS VSLPTTTFNELVTQRKHNEVVMVDFYSPWCHPCQVLMPEWKR MART
LTGLINVGSIDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYSLRIWGLG
FLPQVSTDLTPTQTFSEKVLQKNHWVIDFYAPWCGPCQNFAP EPELLARMIKGKV KAGKVDC
QAYAQCQKAGIRAYPTVKFYFYERAKRNFQEEQINTRDAKATAALISEKLETLRNQGKRKNDEL

Important features:

Endoplasmic reticulum targeting sequence.

amino acids 744-747

Cytochrome c family heme-binding site signature.

amino acids 158-163

Nt-dnaJ domain signature.

amino acids 77-96

N-glycosylation site.

amino acids 484-487

FIGURE 191

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGAGGACAGAGCAAA
GCCATGAACATCATCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGGGA
GTCGTTGGTGAAGTTTTTCATTCTCTCAGAGGAGAAAACTGTGGCTGGGGAGATTGTTCTCA
TTACTGGAGCTGGGCATGGAAATAGGCAGGCAGACTACTTATGAATTTGCAAAACGACAGAGC
ATATTGGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAACTGCAGCTGAGTGCCGAAA
ACTAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCT
CTCTAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACA
GTATATCCAGCCGATCTTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAA
CATCCTAGGACATTTTTGGATCACAAAAGCACTTCTTCCATCGATGATGGAGAGAAATCATG
GCCACATCGTCAAGTGGCTTCAGTGTGCGGCCACGAAGGGATTTCCTTACCTCATCCCATAT
TGTTCCAGCAAAATTTGCCGTGTGGCTTTCACAGAGGTCTGACATCAGAACTTCAGGCCCTT
GGGAAAACTGGTATCAAAACCTCATGTCTCTGCCAGTTTTTGTGAATACGCGGTTCACCA
AAAATCCAAGCACAAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGTCTGATA
GATGGAATACTTACCAATAAGAAAATGATTTTTGTTCCATCGTATATCAATATCTTCTGAG
ACTACAGAAGTTTCTTCTGAAACGCGCCTCAGCGATTTTTAAATCGTATGCAGAATATTCAAT
TTGAAGCAGTGGTTGGCCACAAAATCAAAATGAAATGAATAAAATAAGCTCCAGCCAGAGATG
TATGCATGATAATGATATGAATAGTTTCGAATCAATGCTGCAAGCTTTATTTACATTTTT
TCAGTCTGATAATATTAAAAACATTGGTTTGGCACTAGCAGCAGTCAAACGAACAAGATTA
ATTACCTGCTTCTGTTTTCTCAAGAATATTTACGTAGTTTTTCATAGGCTGTGTTTTCTCTT
TCATGCCTCTTAAAAAATTCTGTGCTTACATAAACATACITAAAAGGTTTTCTTTAAGATAT
TTTATTTTTCCATTTAAAGGTGGACAAAAGCTACCTCCCTAAAAGTAAATACAAAGAGAAT
TATTTACACAGGAAGGTTTAAAGACTGTTCAAGTAGCATTCCAATCTGTAGCCATGCCACAG
AATATCAACAAGAACACAGAATGAGTGCACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTTT
ATCTCAACCTGGACATATTTTAAAGATTGACATTGAAAGATTTCCCTAGCCTCTTCTCTTT
TCATTAGCCCCAAAACGGTGCAACTCTATTCTGGAATTTATTACTTGATTCTGTCTTCTGTAT
AACTCTGAAGTCCACAAAAGTGGACCCTCTATTTTCTCCTCTTTTATAGTCTTATAAGA
TACATTATGAAGGTGACCGACTCTATTTTAAATCTCAGAAATTTAAGTTCTAGCCCCATGA
TAACCTTTTTCTTGTAAATTTATGCTTTTATATATCCTTGGTCCAGAGATGTTTAGACAA
TTTAGGCTCAAAAATTAAGCTAACACAGGAAAAGGAAGTGTACTGGCTATTACATAAGAA
CAATGGACCCAAGAGAAGAA

FIGURE 192

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409

<subunit 1 of 1, 300 aa, 1 stop

<MW: 33655, pI: 9.31, NX(S/T): 1

MNIILEILLLLITIIYSYLESLVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTEFAKRQSI
LVLWDINKRGVEETAABECLKGVTAHAYVVDSCSNREEIYRSLNQVKEVGDVTIVVNNAGTV
YPADLLSTKDEEITKTFEVNILGHFWITKALLPSMMERNHGHIVTASVCGHEGIPYLIPYC
SSKFAAVGFHRGLTSELQALGKTGIKTSCLCPVFVNTGFTKNPSTRLLWPVLETDEVVRSLLD
GILTNNKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK

Important features:

Signal peptide:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-33 and 58-61

Short-chain alcohol dehydrogenase family protein

amino acids 165-202, 37-49, 112-122 and 210-219

FIGURE 193

CGGCGGCGGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCCAGCAGG
ATGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGGCCAGCCCCCGGGGCG
AGGATGACCAAGGCCCGGCTGTTCGGCTGTGGCTGGTGCTGGGGTTCGGTGTTTCATGATCCT
GCTGATCATCGTGTACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGCACAGTCCTTCT
CTAGGCCGCACACGGGGCCCGCTGCCACGCCCGGGCCGGACAGGGACAGGGAGCTCACG
GCCGACTCCGATGTGCAGAGATTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGA
CCTTCCAGAAAGGAGACGGAGCAGCCGCTGCGCCGGGGAGCATGGAGGAGAGCGTGAGAG
GCTACGACTGGTCCCCGCGCAGCCCGGCGCAGCCAGACCAGGGCCGGCAGCAGGCGGAG
CGGAGGAGCGTGCTGCGGGGCTTCTGCGCCAACCTCCAGCCTGGCCTTCCCCACCAAGGAGCG
CGCATTTCGACGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGGACGACCGGCACGGGG
CCATCTACTGCTACGTGCCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTG
AGCGGAAGCCTGTGTCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCGAGCA
CGTGCAACAACGCCAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCT
CCCGCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCTCTTCGTGCGCGACCCC
TTCGTGCGCTGATCTCCGCTTCCGCGAGCAAGTTCGAGCTGGAGAACGAGGAGTTCTACCG
CAAGTTCGCGGTGCCATGTGCGGCTGTACGCCAACACACAGCCTGCCCGCTCGGCGC
GCGAGGCCCTTCGCGCTGGCCTCAAGGTGTCTTCGCCAACTTCATCCAGTACCTGCTGGAC
CCGCACACGGAGAAGCTGGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCTCTGCCA
CCCGTGCCAGATCGACTACGACTTCTGTGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGC
AGCTGCTGCACTACTCCAGGTGGACCGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGG
ACCGCCAGCAGCTGGGAGGAGACTGGTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCT
GTATAAACTCTACGAGGCCGACTTTGTCTCTTCGGCTACCCCCAAGCCGAAAACTCTCCTC
GAGACTGAAGCTTTCGCGTTGCTTTTCTCGCGTGCCCTGGAACCTGACGCACGCGCACTCC
AGTTTTTTTATGACCTACGATTTTGCAATCTGGGCTTCTTGTTCACCTCCACTGCGCTATCC
ATTGAGTACTGTATCGATAATTGTTTTTAAAGATTAATATATTTTCAGGTATTTAATACGA

0997864-101601

FIGURE 194

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56112
<subunit 1 of 1, 414 aa, 1 stop
<MW: 48414, pI: 9.54, NX(S/T): 4
MTKARLFRLWLVLGSVFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRELT
DSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRGYDWSPRDARRSPDQGRQQAER
RSVLRGFCANSSLAFPTKERAFDDIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRMIVLS
GSLLRGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPF
VRLISAFRSKFELNEEFYRKFAVPMRLRYANHTSLPASAREAFRAGLKVSFANFIQYLLDP
HTEKLAPFNEHWRQVYRLCHPCQIDYDFVGKLETLDDEAQLQLQVDRQLRFPPSYRNRT
ASSWEEDWFAKIPLAWRQQLYKLYEADFVLFGYPKPENLLRD

Important features:

Signal peptide:

amino acids 1-31

N-glycosylation sites.

amino acids 134-137, 209-212, 280-283 and 370-373

TNFR/NGFR family cysteine-rich region protein

amino acids 329-332

FIGURE 195

TCGGGCCAGAAATTCGGCACGAGGCGGCACGAGGGCGACGGCCTCACGGGGCTTTGGAGGTGA
AAGAGGCCCAGAGTAGAGAGAGAGAGACCGACGTACACGGGATGGCTACGGGAACGCGCT
ATGCCGGGAAGGTGGTGGTCTGTGACCGGGGCGGGCGCGGCATCGGAGCTGGGATCGTGCGC
GCCTTCGTGAACAGCGGGGCCGAGTGGTTATCTGCCGACAAGGATGAGTCTGGGGGCCGGC
CCTGGAGCAGGAGCTCCCTGGAGCTGTCTTTATCCTCTGTGATGTGACTCAGGAAGATGATG
TGAAGACCCTGGTTTCTGAGACCATCCGCCGATTGGCCGCCCTGGATTGTGTTGTCAACAAC
GCTGGCCACCACCCACCCCCACAGAGGCCTGAGGAGACCTCTGCCCAGGGATTCCGCCAGCT
GCTGGAGCTGAACCTACTGGGGACGTACACCTTGACCAAGCTCGCCCTCCCTACCTGCGGA
AGAGTCAAGGGAATGTCATCAACATCTCCAGCCTGGTGGGGGCAATCGGCCAGGCCAGGCA
GTTCCCTATGTGGCCACCAAGGGGGCAGTAACAGCCATGACCAAAGCTTTGGCCCTGGATGA
AAGTCCATATGGTGTCCGAGTCAACTGTATCTCCCAGGAAACATCTGGACCCCGCTGTGGG
AGGAGCTGGCAGCCTTAATGCCAGACCCTAGGGCCACAATCCGAGAGGGCATGCTGGCCAG
CCACTGGGCCGCATGGGCCAGCCCGCTGAGGTGCGGGGCTGCGGCAGTGTTCTGGCCTCCGA
AGCCAACTTCTGCACGGGCATTGAACTGCTCTGTGACGGGGGTGCAGAGCTGGGGTACGGGT
GCAAGGCCAGTCGGAGCACCCCGTGGACGCCCGGATATCCCTTCTTGAATTTCTCTCATTT
CTACTTGGGGCCCCCTTCTAGGACTCTCCACCCCAAACCTCAACCTGTATCAGATGCAGC
CCCCAAGCCCTTAGACTCTAAGCCAGTTAGCAAGGTGCCGGGTACCCCTGCAGGTTCCCAT
AAAAACGATTTGCAGCC

00978561-101601

FIGURE 196

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56045

<subunit 1 of 1, 270 aa, 1 stop

<MW: 28317, pI: 6.00, NX(S/T): 1

MATGTRYAGKVVVVTGGGRGIGAGIVRAFNVS GARVVICDKDES GGRAL EQELPGAVFILCD
VTQEDDVKTLVSETIRRFGRILDCVVNNAGHHPPQRP EETSAQGFRQLLELNLLGTYTLTKL
ALPYLRKSQGNVINISSLVGAIGQAQAVPYVATKGAVTAMTKALALDESPYGVRVNCISPGN
IWTPLWEELAALMPDPRATIREGMLAQPLGRMGQPAEVGAAAVFLASEANFCTGIELLVTTGG
AELGYGCKASRSTPVDAPDIPS

Important features:

N-glycosylation site.

amino acids 138-141

Short-chain alcohol dehydrogenase family protein

amino acids 10-22, 81-91, 134-171 and 176-185

09978564-101601

FIGURE 197

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATGGACTGGCCTCACAACTG
CTGTTTCTTCTTACCATTTCATCTTCCTGGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAA
GAGGAAAGGGCAAGGGCGGCCTGGGCCCCCTGGCCCCCTGGCCCTCACCAGGTGCCACTGGACC
TGGTGTCA CGGATGAAAACCGTATGCCCGCATGGAGGAGTATGAGAGGAACATCGAGGAGATG
GTGGCCAGCTGAGGAACAGCTCAGAGCTGGCCAGAGAAAGTGTGAGGTCAACTTGCAGCT
GTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCAGCC
GTATCCCCGTGGACCTGCCGGAGGCACGGTGCCCTGTGTCTGGGCTGTGTGAACCCCTTCACC
ATGCAGGAGGACCGCAGCATGGTGAGCGTGCCGGTGTTACGCCAGGTTCCCTGTGCGCCGCCG
CCTCTGCCCGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCG
CTGTGGGCTGCACCTGCATCTTCTTGAATCACCTGGCCCAGAAGCCAGGCCAGCAGCCCCGAGA
CCATCCTCCTTGACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAA
GCAAG

097564-10101

FIGURE 198

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59294
<subunit 1 of 1, 180 aa, 1 stop
<MW: 20437, pI: 9.58, NX(S/T): 1
MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGPHQVPLDLVSRMKPYARMEEY
ERNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPRIIPVDLPEARCLCL
GCVNPFTMQEDRSMVSVPVFSQVPVRRRLCPPPPRTGPCRQRAVMETIAVGCTCIF

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 75-78

Homologous region to IL-17

amino acids 96-180.

097564.107604

FIGURE 199

GCGCCGCCAGGCGTAGGCGGGGTGGCCCTTGCGTCTCCCGCTTCCTTGAAAAACCCGGCGGG
CGAGCGAGGCTGCGGGGCCGGCCGCTGCCCTTCCCCCACTCCCGCCGAGAAAGCCTCGCTCG
GCGCCCAACATGGCGGGGTGGGCGCTGCGGCCCGCAGCTAACGGCGCTCCTGGCCGCGTGGAT
CGCGGCTGTGGCGGCAGCGCAGGCCCGCAGGAGGCCGCGCTGCCGCCGAGCAGAGCCGGG
TCCAGCCCATGACCGCCTCCAACCTGGACGCTGGTGATGGAGGGCGAGTGGATGCTGAAATTT
TACGCCCCATGGTGTCCATCCTGCCAGCAGACTGATTCAGAAATGGGAGGCTTTTGCAAAGAA
TGGTGAAATACCTCAGATCAGTGTGGGGAAGGTAGATGTCTATTCAAGAACAGGTTTGAGTGT
GCCGCTTCTTTGTCAACACTCTCCAGCATTTTTCATGCAAAGGATGGGATATTCGCCCT
TATCTGGGCCAGGAATCTTCGAAGACCTGCAGAATTATACTTTAGAGAAGAAATGGCAATC
AGTCGAGCCTCTGACTGGCTGGAAATCCCCAGCTTCTCTAACGATGTCTGGAATGGCTGGTC
TTTTTAGCATCTCTGGCAAGATATGGCATCTTCACAACTATTTACAGTGACTCTTGGAAT
CCTGCTTGGTGTCTTATGTGTTTTTCGTCTATAGCCACCTTTGGTTTTTGGCCTTTTTATGGG
TCTGGTCTTGGTGGTAATATCAGAATGTTTTCTATGTGCCACTTCCAAGGCATTATCTGAGC
GTTCTGAGCAGAATCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAG
GAGGAAAAAGATGATTCAAATGAAGAAGAAAAACAAAGACAGCCTTGTAGATGATGAAGAAGA
GAAAGAAGATCTTGGCGATGAGGATGAAGCAGAGGAAGAAGAGGAGGACAACTTGGCTG
CTGGTGTGGATGAGGAGAGAAGTGAGGCCAATGATCAGGGGGCCCCAGGAGAGGACGGTGTG
ACCCGGGAGGAAGTAGAGCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCTGCCAGC
TGACACAGAGGTGGTGAAGACTCCTTGAGGCAGCGTAAAAGTCAGCATGCTGACAAGGGAC
TGTAGATTAAATGATGCGTTTTCAAGAATACACACCAAAACAATATGTCAGCTTCCCTTTGG
CCTGCAGTTTGTACCAAAATCCTTAATTTTTCTGAAATGAGCAAGCTTCTCTTAAAGATGCT
CTCTAGTCATTTTGGTCTCATGGCAGTAAGCCTCATGTATATAAGGAGAGTCTTCCAGGTGT
GACAAATCAGGATATAGAAAAACAACGTAAGTGTGGGATCTGTTTGGAGACTGGGATGGGAA
CAAGTTCATTTTACTTAGGGGTGAGAGAGTCTCGACCGAGGAGGCCATTCCAGCTCCTAATC
AGCACCTTCCAGAGACAAGGCTGCGAGGCCCTGTGAAATGAAAGCCCAAGCAGGAGCCTTGGCT
CCTGAGCATCCCCAAAGTGTAACGTAGAA3CCTTGATCCTTTTCTTGTGTAAAGTATTTAT
TTTTGTCAAATTGCAAGAAACATCAGGCACACAGTGCATGAAAAATCTTTACAGCTAGAA
ATTGAAAGGGCCTTGGGTATAGAGAGCAGCTCAGAAGTCATCCAGCCCTCTGAATCTCCTG
TGCTATGTTTTTATTTCTTACCTTTAATTTTTCCAGCATTTCCACCATGGGCATTACGGCTCT
CCCACTCTTCACTATTATCTCTTGGTCAGAGGACTCCAATAACAGCCAGGTTTACATGAAC
TGTGTTTTGTTTCTGACCTAAGGGGTTTAGATAATCAGTAACCATAAACCCCTGAAGCTGT
GACTGCCCAAACATCTCAAATGAAATGTTGTGGCCATCAGAGACTCAAAGGAAGTAAGGATT
TTACAAGACAGATTAAAAAAAATTTGTTTTGCCAAAATATAGTTGTTGTTGATTTTTTTT
AAGTTTTCTAAGCAATATTTTTCAAGCCAGAAGTCTCTAAGTCTTGCCAGTACAAGGTAGT
CTTGTGAAGAAAAGTTGAATACTGTTTTGTTTTCTAAGGCGTTCCCTGGGTCTTGAAC
TACTTTAATAATAACTAAAAAACCACTTCTGATTTTCCTTCAGTGATGTGCTTTTGGTGAAA
GAATTAATGAACCTCCAGTACTGAAAGTGAAGGATTGATTTTGTGTTCCATCTTCTGTAATC
TTCCAAAGAATTATCTTTGTAAATCTCTCAATACTCAATCTAGTAAGTACCAGGGAG
GCTAATTTCTTT

0978564-101601

FIGURE 200

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56433
<subunit 1 of 1, 349 aa, 1 stop
<MW: 38952, pI: 4.34, NX(S/T): 1
MAGGRCGPQLTALLAAWIAAVAATAGPEEAALPPEQSRVQPMTASNWTLVMEGEWMLKFYAP
WCPSCQQTDSEWEAPAKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGIFRRYRG
PGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMMSGMAGLFSISGKIWHLHNYFTVTLGIPAW
CSYVFFVIATLVFGLFMGLVLVVISFCFYVPLPRHLSESEQNRRSEEAHRAEQLQDAEEEEK
DDSNEEENKDSLVDDEEEKEDLGDEDEAEEDNLAAGVDEERSEANDQGPPEGEDGVTRE
EVEPEEAEEGISEQPCPADTEVVEDSLRQRKSKHADKGL

Important features:

Signal peptide:

amino acids 1-22

Transmembrane domain:

amino acids 191-211

N-glycosylation site.

amino acids 46-49

Thioredoxin family proteins. (homologous region to disulfide isomerase)

amino acids 56-72

Flavodoxin proteins

amino acids 173-187

00075531-42557600

FIGURE 201

ATCTGGTTGAACTACTTAAGCTTAATTTGTTAAACTCCGTAAGTACCTAGCCACATGATT
TGACTCAGAGATTTCTTTTGTCCACAGACAGTCATCTCAGGGGCAGAAAAGAAAGAGCTCC
CAAATGCTATATCTATTCAGGGGCTCTCAAGAACAAATGGAATATCATCTCTGATTAGAAAAAT
TTGGATGAAGATGGATATATACTCAATTACACTTCGACTCTCAAAGCAATACCAGGATAGCTGT
TGTTTCAGAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCTCATGTGTAAATTTTGG
GAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCTGGGTACCATGGGGGTTCTTTCC
AGCCCTTGTCTCTCAATTTGGATTATATATGAGAAGAGCTGTTATCTATTGAGCATGTCACT
AAATCTCTGGGATGGAAGTAAAGACAATGCTGGCAACTGGGCTCTAATCTCCTAAAGATAG
ACAGCTCAAAATGAATGGGATTTATAGTAAAAACAAGTGTCTTCCCAACTGATAATTCATTT
TGGATAGGCCCTTTCTCGGCCCCAGACTGAGGTACCATGGCTCTGGGAGGATGGATCAACATT
CTCTTCTAACTTATTTAGATCAGAACCACAGCTACCCAGAAAAACCCATCTCCAATTTGTG
TATGGATTACGTTGTCAGTCATTTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTTGT
GAGAAGAAGTTTTCAATGTAAAGAGGAAGGGTGAGAAGGAGAGAGAAATATGTGAGGTAGTA
AGGAGGACAGAAAAACAGAACAGAAAAGAGTAACAGCTGAGGTCAAGATAAAATGACAGAAATG
TTTAGAGAGCTTGGCCAACCTGTAATCTTAAACCAAGAAATTGAAGGGAGAGGCTGTGATTCT
GTATTTGTGCACTACAGGTAGGCTAGTATTATTTTCTAGTTAGTAGATCCCTAGACATGG
AATCAGGGCAGCCAAGCTTGAGTTTTATTTTTTATTATTATTATTGATAGAGTGGGTCT
CACTTTTGTATCCCAAGGCTGGAGTGCAGTGGCACAATCTCGACTCACTGCAGCTATCTCTCGC
CTCAGCCCCCTCAAGTAGCTGGGACTACAGGTGCATGCCACCATGCCAGGCTAATTTTTGGTG
TTTTTTGTAGAGACTGGGTTTTGCCATGTTGACCAAGCTGGTCTCTAACTCCTGGGCTTAAG
TGATCTGCCCGCCTTGGGCTCCCAAAGTGTCTGGGATTACAGATGTGAGCCACCACACCTGGC
CCCAAGCTTGAATTTTCATTCTGCCATTGACTTGGCATTACCTTGGGTAAGCCATAAGCGA
ATCTTAATTTCTGGCTCTATCAGAGTTGTTTCATGCTCAACAATGCCATTGAAGTGCACGGT
GTGTTGCCACGATTTGACCTTCAACTTCTAGCAGTATCATGATTATGAATGAGGGTGAAAT
ATATTTCTGAATAGCTAAATGAAGAAATGGGAAAAAATCTTACCACAGTCAGAGCAATTTT
ATTATTTTCATCAGTATGATCATAATTATGATTATCATCTTAGTAAAAAGCAGGAACCTCTA
CTTTTTCTTTATCAATTAATAGCTCAGAGAGTACATCTGCCATATCTCTAATAGAATCTTT
TTTTTTTTTTTTTTTTTTTGGAGACAGAGTTTCGCTCTTGTGCCCCAGGCTGGAGTGCACCGG
CACGATCTCGGCTCACGCCAACCCTCCGCCCTCGGGTTCAAGCAATTTCTCTGCCTCAGCCT
CCCAAGTAGCTGGGATTACAGTCAGGCACCAACCACCCGGCTAAATTTTGATTTTTTTTGT
AGAGACAGGGTTTTCTCCATGTCCGTCAGGGTAGTCCCGAACTCCTGACCTCAAGTGATCTGC
CTGCCCTCGGCTCCCAAGTGTCTGGGATTACAGGCGTGAGCCACTGCACCCAGCCTAGAACTCT
TGTATATATGTAATTTGAGGGAACTGCTCTCATAGGAAAGTTTTCTGCTTTTTAAATACA
AAAATACATAAAAATACATAAAATCTGATGATGAATATAAAAAGTAACCAACCTCATTGGA
ACAAGATTAAACATTTTTGGAATATGTTTTATTAGTTTTGTGATGATGATGTTTTTACAATTTTT
ACCATTTTTTTTTCAGTAATTTACTGTAATAATGGTATTTATGGAATGAAACTATATTTTCTCAT
TGTGATTTTGTCTTATTTTTTTTTCATACCTTTCCCACTGGTGTCTTTTTTATTTCCAATGGATA
TTTCTGTATTACTAGGGAGGCATTTACAGTCTCTAATGTTGATTAAATATGTGAAAGAAAT
TGTACCAATTTTACTAAATATGACAGTTTAAATGGATGATTTTATGTTATGTGGATTTCAT
TTCAATAAAAAAAACCTCTTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

0997554.101501

FIGURE 202

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912
<subunit 1 of 1, 201 aa, 1 stop
<MW: 22563, pI: 4.87, NX(S/T): 1
MEYHPDLENLDEDGYTQLHFDSQSNTRIAVVSEKGSAAAPPWRLIAVILGILCLVILVIAV
VLGTMGVLSPPCPNWIIEKSCYLFMSLSNSWDGSKRQCWQLGSNLLKIDSSNELGFIVKQ
VSSQPDNSFWIGLSRPQTEVPWLWEDGSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQL
CSVPSYSICEKKFSM

Important features:

Type II transmembrane domain:

amino acids 45-65

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 197-200

N-myristoylation sites.

amino acids 35-40 and 151-156

Homologous region to LDL receptor

amino acids 34-67 and 70-200.

FIGURE 203

GGAAGGGGAGGAGCAGGCCACACAGGCCAGGCGCGGTGAGGGACCTGCCAGACCTGGAGGGTCTCGCTCTGTCA
 CACAGGCTCGAGTGCAGTGTGTGATCTTGGCTCATCGTAACCTCCAGCTCCCGGGTTCAAGTGATTCTCATGCC
 TCAGCCTCCGAGTAGCTGGGATTACAGTGGTGACTTCCAAGAGTGACTCCGTGGAGGAAATAGCTCTCCGAG
 TCGCTGCTGCAGACGACACTGTTCTGCTGTGAGTGTGCTTCTCTGGTCCAAGTGTGCCACCGGAGGGGCCACAGG
 GAAGACTTTTCGCTTCTGCAGCCAGCGGAAACAGACACAGGAGCAGCTCCACTACACAAACCCACACAGACCTG
 CGCTATCTCCATCGAGAACTCCGAGAGGCGCTTCAGTCCATGCCCTTTCCCTGCAGCCACCCCTGCTTCCGGA
 TCTTTCCTGACCCAGGGGCTTACCACTTCTGCTCTACTGGAACCGACACTGTCTGGGAGATTACATCTTTCTC
 TATGGCAAGGTGACTTCTGTGTGAGTGACAAAGCCTTAGCCTCTCTGCTTCCAGCACCGAGGAGAGAGCCTG
 GCTCAGGGCCCCCGCTGTAGCCACTTCTGTGACCTCTGTGGAGCCCTCAGAACATCAGCCTGCCAGTGCCTG
 GCCAGCTTCACTTCTCTCTTCACAGTCTCTCCACACCGCGCTCACAATGCTCGTGGAGATGTGCGAGCTC
 AAAAGGGACCTCCAGTGTCTCAGCCAGTTCCTGAAGCATCCCAGAAGGCTCAAGGAGGCCCTCGGCTGCCCCC
 GCCAGCCAGCAGTTGCAGAGCTTGGAGTCGAAATGACCTCTGTGAGATTATGAGGGGACATGGTGTCTTCGAG
 GAGGACCGGATCAACGCCAGGTTGGAGGCTCCAGCCACAGCCGCGCTCCAGGACCTGCACATCCTCACTCCCGG
 CAGGAGGAGGAGCAGAGCGAGATCATGGAGTACTCGGTGCTGTGCTCGCAACACTCTTCCAGAGGACGAAAGGC
 CGGAGCGGGGAGCTGAGAAGAGACTCTCTCTGGTGGACTTCAGCAGCCAGGCCCTGTTCAGGACAAGAATTC
 AGCCAAAGTCTTGGGTGAGAAGTCTTGGGGATTGTGGTACAGAACACCAAGTAGCCAACTCAGCGAGCCCGTG
 GTGCTCACTTCCAGCACAGCTACAGCCGAGAAGTGTGACTCTGCAATGTGTGTTCTGGGTTGAAGACCCCA
 TTGAGCAGCCCGGGGACTGGAGCAGTGTGGGTGTGAGACCGTCAGGAGAGAAACCAACATCTGCTTCTGCG
 AACCACTTGACTTACTTTGTGAGTGTGATGGTCTCTCGTGGTGGAGTGGAGCGCTGTTCAGGACAAGACTCTGAGC
 CTCTCTCTTACGTGGGCTGTGCTGCTCTGCGCTGGCCTGCTTGTCAACATTGCCGCTTACTCTGTCTCCAGG
 GTGCCCCGTGGGAGGAAACCTCGGACTACACCATCAAGGTGACATGAACCTGTGCTGCTGGCTGCTGCTCTC
 CTGCTGGACAGAGCTTCTGCTCAGCGAGCCGGTGGCCCTGACAGGCTCTGAGGCTGGCTGGCGAGCCAGTGGC
 ATCTTCTGCTACTTCTCCGTCTCACTTGGCTTCTTCTGGATGGGCTCGAGGGGTACAACCTCTACCGACTCTG
 GTGAGGCTCTTGGGACCTTGTGCTTCCCTGGCTCACTACTCAAGCTGAGCGCCATGGGCTGGGGCTTCCCATCTTT
 CTGCTGAGCTGTGCGCTTGGTGGATGTGGACACTATGGCCCATCATCTTGGCTGTGATAGGACTTCAGAG
 GCGCTTACTTACCTTCCATGTGCTGGATCCGGACTCCCTGTGTGACTACATCACCAACCTGGGCGCTTTCAGC
 CTGTTGTTTCTGTTCACACTGGCCATGTAGCCACACTATGGTGGTGAGTCTGGCGCTGCCGCCACACCCAA
 AAGTGGTACATGTGCTCAGACTGTGCGCTCAGCCTGTGCTTGGGCTGGCCTGGGCTTGTATCTTCTCTCTC
 TTGTGCTCTGGCACCTCTGACCTTGTGCTCTTACTCTTTTCACTCATCACTCTTCCAAAGCTTCTCTATC
 TTATCTGTGACTGTCTCATGCGGCTGACGCGCCGGGTGGGCTTCCCTCTGAAAGACCACTCAGACAGCGCC
 AGGCTCCCATCAGCTCGGCGAGCACTCGTGCAGCCGATCTAGGCTCCAGCCCACTGGCATGTGATGAAG
 CAGAGATGCGGCTGTGCACTGCTGCTGTGCGCCCGAGCCAGCCAGCCAGTCCAGCCGACACT
 TTGGAAGCCCAACAGCACTGGAGAGATGGGCGGTGGCCATGTGGAGCGACTCCCGGCTGGGCTTTTGAATTG
 GCTCTGGGACTACTCGGCTCTCACTCAGCTCCACGGGACTCAGAAGTGGCGCGGCTGTCTGCTAGGTAAGT
 TCCCAAGCTGTGCCAACCCAGCTGGAGGCTGGGTCTCTCTTACAACCCCTGGGCGCAGCCCTCATGTCTGG
 GGCGAGGCTTGGATCTTGAAGTCTTGAAGGTCTGGCACATCTTAACTCTGTGCGCTTCTGGGACAGAAATGTGGCTCA
 GTTGTCTGTCTCTGTGGTCACTCTGAGGGCACTCTGCATCTCTGTCAITTTAACTCTAGTGGCACCCAGG
 CGAATGGGGCCAGGGCAGACTTCAGGGCCAGAGCCCTGGCGGAGGAGGCGCTTTGCCAGGACACAGCAGC
 AGCTCGCTACTCTGTAGCCAGCGCCCTCCCTCCCTCAGCCCCAGTCTCTCTCATCTTCTCTGGGGTTT
 TCTCTCTCCCGAGGCTCTTGTGCTCTGTTTACAGCTGGGGGTCCCCGATTCAATGCTGTTTGTGGGA
 GTGGTTTCCAGGAGCTGCTGGTGTCTGCTGTAAATGTTTGTCTACTGCACAAGCTCGGCTGGCCCTTAGGACA
 GGTCTGGTAGCAGTGGCTGGGCTGGGCTAGGTGCTCTCTGTGCTTCTGGGCTTTGATAGAGTGCATTGGCCTTG
 CTACCCCTGACCAAGCAGCAGCTCAGAGGGGCGCTCAGGCTCTCTGAAGCGCTTCTGTGGCAAGAACTGTGGA
 CCATCGCAGTCCCGTCTGCTTTTCCATCCCACTCCAAAGGACTGAGACTGCTCTGTGTGACTGCTGGCCTTA
 GAGCTGTGACTCTCTTAAAGAGTCTCTCAAGCCCCAAATAGCTCCAGGGCGCTTGGCGGCCCATATGTGT
 TAAATTTGTCTCAAAACACACACGGGTAGATTGCTGGCCTTGTGTAGTGGTAGGACACAGATGACCGACTG
 GTCACTCTCTGTGCCAATCTTCACTGTGATGTGAGGCGTGGTGAAGCAGAACTCTTGGAGCTACAGGGACA
 GGGAGCACTCACTTCTGCTGGGAATCTGGAAGACTCTTCTGAGGAGTCAAGCTTCAATCTTGAACCTTGAAGT
 GGGAGAGATGTTCTTTTACGTACCAATTTCTTTGTCTTTTGATATTTAAAGAAAGTACATGTTTCACTGTGAGA
 ATTGTGAAGCTGTAGAAGAGATTCAAGAGAGAAAATAAAATCAGCTGTGTGTAATCGCTTACGAAAAA
 AA

09978564.101601

FIGURE 204

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921
<subunit 1 of 1, 693 aa, 1 stop
<MW: 77738, pI: 8.87, NX(S/T): 7
MTPQSLQLQTTLFLLSLLFLVQGAHGRGHREDFRFCSSQRNQTHRSSSLHYKPTPDLRISIENSE
EALT VHAPFPAAHPASRSPDPGRGLYHFCIYWNRHAGRLHLLYGKRDFLSDKASSLLCFQH
QEESLAQGPPLLATSVTSWSPQNISLPSAASF TFSFHSPPHTAAHNASVDMCELKRDLQLL
SQFLKHPQKASRRPSAAPASQQLQSLESKLTSVRFMGDMVSFEEDRINATVWKLQPTAGLQD
LHIHSRQEEQSEIMEYSVLLPRTL FQRTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGE
KVLGI VQNTKVANLTEPVVLT FQHQLQPKNVTLCQVFWVEDPTLSSPGHWSSAGCETVRE
TQTCSCFNHLTYFAVL MVSSVEVD AVHKHYLSLLSYVGCVVSA LACLV TIAAYLC SRVPLPC
RRKPRDYTIKVH MNLLLA VFLDTSFLLSEPVALTGSEAGCRASAI FLHFSLLTCLSWMGLE
GYNLYRLVVEVF GTYVPGYLLKLSAMGWGFPI FLVTLVALVDVDNYGPI ILAVHRTPEGVIY
PSMCWIRDSLVS YITNLGLFSLVFLFNMA MLATMVVQILRLRPHTQKWSHVLTLGLSLVLG
LPWALIFFSFASGTFQLVVLYLFSIITSFQGFLIFIWYSMLRQARGGPSPLKSNSDSARLP
ISSGSTSSSRI

Important features:

Signal peptide:

amino acids 1-25

Putative transmembrane domains:

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590
and 634-657

Microbodies C-terminal targeting signal.

amino acids 691-693

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 198-201 and 370-373

N-glycosylation sites.

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327
and 341-344

G-protein coupled receptors family 2 proteins

amino acids 475-504

09978564-301601

FIGURE 205

TGCCTGGCCTGCCTTGTCAACAATGCCGCTTACTCTGCTTCCAGGTTGCCCTGCCTTGAGA
GGAAANCNTCGGGACTACACNNTCAAGTGACATGAACCTGCTGCTGGCCGTCTTCCTGCTG
GACACGAGCTTCCTGCTCAGCGNAGCCGGTGGCCCTGACAGGCTCTGAAGGCTGGCTGCCGA
GCCAGTGCCATCTTCCTGCACTTCTCCTGCTCACCTGCCTTTCTGGATGGGCCTCGAGGGG
TACAACTCTACCGACTCGTGGTGGAGGTCTTTGGCACCTATGTCCCTGGCTACCTACTCAA
GCTGAGCGCCATGGGCTGGGGCTTCCCCATCTTTCTGGTGACGCTGGTGGCCCTGGTGGATG
TGGACAACTATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAGGGCGTCATCTACCCT
TCCATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATCACCAACCTGGGCCTCTTCAGCCT
GGTGTTTCTGTTCAACATGG

197554.11461

FIGURE 206

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGCTCAGGTCCAGGTTTTGCTTTGA
 TCCTTTTCAAAAACTGGAGACACAGAAGAGGGCTCTAGGAAAAAGTTTTGGATGGGATTATGTGGAACTACCCCT
 GCGATTTCTGTCTGCAGAGCAGGCTCGGCGCTTCCACCCAGTGCAGCCTTCCCTTGGCGGTGGTGAAGAGAC
 TCGGAGGTGCTGCTTCCAAGTGCCCGCGTGGAGTGAGCTCTCACCCAGTCAAGCCAAATGAGCCTCTTTGCGGC
 TTCTCTGCTGACATCTGCCCTTGGCCGCGGACAGAGCAGGGGACTCAGCGGGAATCCAACCTGAGTAGTAAATTC
 AGTTTTCCAGCAACAAGGAACAGAACGGAGTACAGATCCTCAGCATGAGAGAATTAATTAAGTGTCTACTAATG
 GAAGTATTCACAGCCCAAGGTTTTCTCATACTTATCCAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAG
 AGGAAATGTATGGATACAACTTACGTTTGTATGAAGATTGGGCTTGAAGACCCAGAAGATGACATATGCAAGT
 ATGATTTTTGTAGAAGTTGAGGAACCCAGTGTATGGAATATATTAGGGCGCTGGTGGTTCTGGTACTGTACAG
 GAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTGTATCTGTATGAATATTTTCTGTGAACCCAGGT
 TCTGCATCCACTACAACATTTGTCATGCCAATTCACAGAAGCTGTGAGTCCCTCAGTGCTACCCCTTCAGCTT
 TGCCACTGGACCTGCTTAATAATGCTATAAATGCCCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACAG
 AGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAAGCTTGGCACTTCTGGCAAGGCTTTGTTTTGGAA
 GAAATCCAGAGTGGTGGATCTGAACCTTCAACAGAGGAGGTAAATATACAGCTGCACACCTCGTAACCTCT
 CAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCAATTTTGCCAGGTTGTCTCTGGTTAAACGCTGTG
 GTGGAACTGTGCCCTGTTGTCTCCAAATTTGCAATGAATGTCAATGTGTCCCAAGCAAGTTACTAAAAATACC
 ACGAGGTCTCTCAGTTGAGACCAAGACCGGTGTGAGGGGATGCACAAATCACTCACCGACGTGGCCCTGGAGC
 ACCATGAGGAGTGTGACTGTGTGTGAGAGGGAGCAGGAGGATAGCGCATCAACCCAGCAGCTCTTGCCCA
 GAGCTGTGCGAGTGCAGTGGCTGATTCTATTAGAGAAGTATGCGTTATCTCCATCTTAACTCAGTGTGTTGCT
 TCCAGGACTCTTTGAGTAGGAGCCTAAGAGGACAGGAGAAAAGGTTCTCAATCGTGAAGAAAATTAATGTTGTAT
 TAAATAGCTCAACAGCTAGTTTTAGAGTTACCATGTACGTATTCATAGCTGGGTTCTGTTATTCAGTCTTTCT
 GATACGCTTAGGGTAACTGTGAGTACAGGAAAAAACTGTGCAAGTGAGCACTGATTCCGTGCTCTGCTTAAAC
 TCTAAAGCTCCAATGCTGGGCTAAATATGATAAAATCTGGATTTTTTTTTTTTTTTTGTCTCATATTCACAT
 ATGTATAACCAAGAACCTCTATGACTCAAACTGTGTTTTTAAAGGAAGTATTTGCTATGAATTAACATGT
 GTCATGCTGATAGCAGAGCTGGATTTTTCATATTTCTATTAAATTTCTGCCATTTAGAGAAGAGAACTACA
 TCTATGTTTTGGAAGATGAATAACTGAAAGAGAGTGGCCTTATCTTCACTTATCGATAAGCTCAGTTTATTGT
 TTTCAATGTGTACATTTTTATATCTCCTTTTGACATATAACTGTGGCTTTCTTAATCTTGTAAATATATCT
 ATTTTTACCAAGGATTTTAATATCTTTTTATGACACTTAGATCACTATTTTTAGCTTGTGTAATTTTTCT
 AAACCAAAATTTGATATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTCA
 TTCTCGTATGGTCTAGAGTTAGATTAATCTGCAATTTTAAAAAATCAATTTGGATAGAATTGGTAGTTGCAAA
 GACTTTTGAATAAATTAATTAATTCATATCTTCCATTTCTGTTATTGGAGATGAATAAAAAAGCACTTATGA
 AAGTAGACATTCAGATCCAGCCATTTACTAACCTATTCCTTTTTTGGGGAATCTGAGCCTAGCTCAGAAAAACAT
 AAAGCACTTTGAAAAGAGCACTGGCAGCTTCTGATAAAGCTGCTGTGCTGTGACAGTAGGAACACATCTATTTA
 TTGTGATGTGTGGTTTTATTATCTTAACTCTGTCCATACACTGTGTATAAATTCATGGATATTTTATGTACA
 GAGATGTCTCTTAAACAGCTTCACTTATGTACTCTGGCAATTTAAAGAAAAATCAGTAAATATTTTGTCTGT
 AAAATGCTCTAATTTGGTGCACTAGTTTAAAAAATAAAAAAAGGTTTTAGGAGTACAGGGTAAATGCGGCC
 ATGTGGCTATTTTTGGGAGAAAATTAATAAAAAAAGGTTTTAGGAGTACAGGGTAAATGCGGCC

09973564-101601

FIGURE 207

MSLFGLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPR
FPHTYPRNTVLVWRLVAVEENVWIIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWC
GSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLL
NNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGKRKSRVVDLNLLEEVRLY
SCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPVSKVTKKYHEVLQ
LRPKTGVRGLHKSLTDVALEHHEECDVCVRGSTGG

Signal sequence:

amino acids 1-14

00072564-101601

FIGURE 208

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACGAGACCTCTACATTCATTTTGGAGA
 AGACTAAATAGTGTGTTCCTCAAGTGGGACACTGAAGAGACAATCTCTATCCCTTTTAAACATAATCCTAAATTTCC
 AAACCTCTCTGGGGCTAGATGGTTTCTCTAAAACCTCTGCCTGTGATGTCACTCTGGATGTTCCAAAGAACCATGTG
 ATCTGGGACTGCACAGACAAGCATTTGACAGAAATCTCTGGAGGTATCTCCACGAGAACCCAGCAGACCTCACCTC
 ACCATTAAACCATACAGACATCTCCCGACGCTCTCTTACAGACTGGACCATCTGGTAGAGATCGATTTAGAG
 TGCACCTGTGTACTCTATTCCACTGGGGTCAAAAAACACATGTGCATCAAGAGGCTGACAGATTAAACCCAGAGG
 TTTAGTGGACTCACTTATTTAAATTCCTTTACAGACTGGACCATCTGGTAGAGATCGATTTAGAG
 TGTGCTCTCAAGCTCTCAGCTCTGAGGCGCAACACATCTTTTCCATCAGAAAAGAGAAATTAACAGAACTGGCC
 CTCTAGCTTTACAGCTCTCAGCTCTGAGGCGCAACACATCTTTTCCATCAGAAAAGAGAAATTAACAGAACTGGCC
 AACATAGAAATCTCTACCTGGGCGCAAACTGTTATTTATCGAAATCTTGTATGTTTATATTCATATTCAATAGAGAA
 GATGCTCTCTAACTTGACAAAGTTAAAGTGCTCTCCCTGAAAGATAACAAATGTCAACGCTCTCTCTACTGTT
 TGGCTCTCTTAACTTGACAACTATATCTCTCAACAACATGATTGCAAAATCAAGAGAGATGATTTTAAATAC
 CTCAACCAATTACAAATTTCTGACCTAAGTGGAAATGCTCTCGTTGTTATATGCTCCCATTTCTTGTGCGCGG
 TGTAAAAATTAATTTCTCCCTACAGATCTCCCTGTAATGCTTTTGTATGCTGACAGAGATTAAGAGTTTACGCTA
 CACAGTAATCTCTCTCAGCATGTGCCCCAAGATGTTTAAAGACATCAACAACTCCAGGAATCTGGATCTGTCC
 CAAAACCTCTTGGCGCAAGAAATTGGGGATGCTAAATTTCTGCAATTTCTCCCGACCTCATCCAATTGGATCTG
 TCTTTCAATTTTGAACCTCAGGCTATCTGTGTCATCTATGAATCTATCAAGCAATTTCTTCTCACTGAAAGCCTG
 AAAATTTCTCGGATCAGAGGATATGCTTTTAAAGAGTTGAAAGCTTTAACTCTCGCCATTACATAATCTTCAA
 AATCTTGAAGTCTTGTATCTTGGCACTAACTTTTATAAAAAATGCTAACCTCAGCATGTTTAAACAAATTTAAAGA
 CTGAAAGTCATAGATCTTTTCACTGTAATAAAATATCACCTTCAGGAGATTCAAGTGAAGTTGGCTTCTGCTCAAAT
 GCCAGAACTTTCTGTAGAAAGTTATGAACCCAGGCTCTGGAACAAATTACATTTATTCAGATATGATAAGTATGCA
 AGGAGTTGCAGATTCAAAAACCAAGAGGCTTCTTTCTATGCTGTTTAAAGAGCTGCTACAAGTATGGGCGAGCC
 TTGGATCTAAGTAAAAATAGTATATTTTGTCAAGTCTCTGATTTTCAAGCATTTCTTCTTCTCAATGCTCT
 AATCTGTGAGAAATCTCATTAGCCAACTCTTAATGGCAGTGAATCCAACCTTTCAGGAGCTGAGATATTTG
 GACTTCTCAACCAACGGCTGATTACTCCATTCAACAGCATTTTGAAGAGCTTCAAAATCGGAAGTCTGAGAT
 ATAAGCAGTAAATAGCCATTATTTTCAATCAGAAGGAATTAATCATATGCTTAACTTACCAAGAGCTTCAAGGTT
 CTGCAGAACTGATGATGAACGACAATGACATCTCTTCTCCACAGCAGGAGCATGGAGAGTGAAGTCTCTTAGA
 ACTCTGGAATTCAGAGGAATCACTTAGATGTTTATGAGAGAGAGGTGATAACAGATACCTTACAATTTCAAG
 AATCTGCTAAATATAGAGGAATAGACATCTTAAATATCCCTAAGTTTCTTGGCTCTGAGAGATTTTGAAGT
 ATGCTCTCAAAATCTAAAGATCTCTTCTTGGCGCAAAATGGCTCAATCTCTTTCAGTGGAGAGAACTCAGGT
 CTAAAGACCTTGAAGAACTTTGACCTCAGCCACAACTGACCACTGTGCTCTGAGAGATTTATCAACTGTCTCC
 AGAAGCTCTCAAGATCTGATTCTTAAGAATAATCAAACTCAGGAGCTGACGAGATTTTCTCAAGATGCTCTC
 CAGTTGCGATATCTGATCTCAGCTCAAAATAAATCCAGATAGATCCAAAGACCACTTCCAGAGATGCTCTC
 AACATCTCAAGATGTTGCTTTTGTGATCATAATCGGTTCTGTGCACTGTGATGCTGTGTGTTTGTCTGGTGT
 GTTAACCATACGAGGAGTGAATCTTCTTACCTGGCCACAGATGTGACTTGTGTGGGCGGAGGAGCACAAAGGC
 CAAAGTGTGATCTCCCTGAGCTGTACACCTGTGAGTTAGATCTGACTAACCTGATCTGTTCTCACTTTCCATA
 TCTGATCTCTCTCTTCTCATGATGATGATGACAGCAAGTCACCTATTTCTGGAGTGTGTGATATATTACCAT
 TCTGTGAGGCGCAAGATAAGGGGATCAGCGTCTAATATCACCAGACTGTGCTATGATGCTTTTATTGTGAT
 GACATTAAGAACCCAGCTGTGACGAGTGGGTTTGGCTGAGCTGTGGGCAAACTGGAAGACCCAGAGAGAA
 CATTTTAAATTTATGCTCTCGAGGAAAGGACTGGTTACCGAGGCGACCAAGTTCTGGAAGAACCTTTCCAGAGCAT
 CAGCTTAGCAAAAAGACAGTGTTTGTGATGACAGACAGTATGCAAGAGCTGAAATTTTAAAGATAGCATTTTAC
 TTGCTCCATCAGAGGCTCATGATGAAAGTGTGATGATTTCTGAGAGCCCTTTCCAGAG
 TCCAGGTTCTCAGCTCGGAAAGGCTCTGTGGAGTTCTGTCTTGTGAGTGAACCAACCCGCAAGCTCAC
 CACTACTCTTGGCAGGTCTCAAAAGACGCTTGGCCACAGACAATCATGTGGCTTATGATCAGGTGTCAAGGAA
 ACGGTCTAGCCCTCTTTGCAAAACCAACTGCTAGTTTACCAAGAGAGGCTGGC

09978564-10101

FIGURE 209

MVFPMWTLKRQILILFNIILISKLLGARWFPKTLPCDVTLDVPKNHVIVDCTDKHLTEIPGG
IPTNTNLTTLTINHIPDISPASFHRLDHLVEIDFRNCNCVPIPLGSKNNMCIKRLQIKPRSFS
GLTYLKSLYLDGNQLLEIPQGLPPSLQLLSLEANNIFSIKKNLTLANIETIYLGQNCYR
NFCYVSYSIEKDAFLNLTCLKVLSLKDNNTAVPTVLPSTLTELYLYNNMIAKIQEDDFNNL
NQLQILDLSGNCPRCYNAPFPCAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPPRWF
KNINKLQELDLSQNF LAKEIGDAKFLHFLPSLIQLDLSFNFELQVYRASMNLSQAFSSLSKSL
KILIRIGYVFKELKSFNLSPLHNLQNLEVLDLGTNFIKIANLSMFKQFKRLKVIDLSVNKIS
PSGDSSEVGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFFKNKEASFMSVNESCYKYGQ
TLDLSKNSIFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRLDLLH
STAFELHKLLEVLDISSNSHYFQSEGITMNLNFTKNLKVQLKMMNDNDISSSTSRTMES
LRTLEFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNSLSFLPSGVFDGMPPNLKNLSL
AKNGLKSFSWKKLQCLKNLETLDLSHNQLTTVPERLSNCSRSLKNLILKNNQIRSLTKYFLQ
DAFQLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLLHNRLCTCDAVWFVWVNVNHTVETIP
YLATDVTCVGPGAHGQSVISLDLYTCELDLTNLILFSLISISVSLFLMVMMTASHLYFWDVW
YIYHFC KAKIKGYQRLISPDCCYDAFIVYDTKDPVTEWVLAELVAKLEDPREKHFNLCL
RDWLPQGQPVLENLSQSIQLSKKTVMFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVILIFLE
KPFQKSKFLQLRKRLCGSSVLEWPTNPQAHFYFWQCLKNALATDNHVAYSQVFKETV

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 840-860

FIGURE 210

GGGTACCATTCTGCGCTGCTGCAAGTTACGGAATGAAAAATTAGAACAAACAGAAACATGGAAAAATGTTCCCTTC
 AGTCGTCAATGCTGACCTGCTTTCTGCTAATATCTGGTTCTGTGAGTTATGCGCCGAAGAAAAATTTTCTA
 GAAGCTATCCCTTGATGAGAAAAAGCAAATGATCTCAGTTATTGCGAGAGTGCAGCAATCGTCGACTAGCAAGAG
 TTCCCAAACCGGTGGGCAAAATGTGTACAGAACTAGACCTGCTGATAATTTTCATCACACATACGAACTGAAT
 CATTTCAAGGGCTGGGCAAAATGTCTCACTAAAAATAATCTAAACCACAAACCCCAATGTACAGCACCAAGACGGAATC
 CCGGTATACAAATCAATAGCTTGGAATATCAGACGCGGGCATTCCTCAACCTAAAAAACCTAAGGGAGTTACTGCT
 TTGGAAGACCAACAGTTTCCCCCAAAATCCCTCTGTTTGCAGAGTCTTTGACAGAACTTAGTCTTAATTTCAAAAAC
 ATATATACACAACTAACTAAAAAGGGGCAATTCAGAGCTTATAAACTTGAAAAATCTCTTATTGGGCTGGAACTGCT
 ATTTTAAACAAGTTTGGGAGAAAACTAACTAGAAGATGGAGTATTGAAACCGCTGACAAATTTGGAGTTGCTAT
 CACTATCTTTCAATCTCTTTTACACGTCGCCACCCAACTGCCAAGCTCCCTACGCAAACTTTTCTGAGCAACA
 CCGAGATCAATACATTTAGTGAAGAAGATTTCAAGGGATTGATAAATTTAAACATTACATAGATTAAAGCGGGAAT
 GTCCGAGGTGCTTCAATGCCCACTTTCCATGCGTGCTTGTGATGGTGGTCTCAATTAATATAGATCGTTTTG
 CTTTTCAAAACCTGACCCAACTCGATACCTAAACCTCTCAGCACTTCCTCAGGAAGATTAAATGCTGCCTGGT
 TTAATAATATGCTCATCTGAAGGTGCTGGATCTTGAATCAACTATTAGTGGGAGAAATAGTCTCTGGGGCAT
 TTTTAAACGATGCTGCCCGCTTAGAAATACTTGACTTGTCTTTAACTATATAAAGGGGAGTTATCCACAGCAT
 TTAATATTTCAGAAACTTCTTAACTTTTGTCTCTACGGGCATTGCAATTAAGAGGTTATGTTTCCAGGAAC
 TCAGAGAAAGATGTTTTCAGCGCTGATGCAGCTTCCAACTTTCGACTATCAACTGGGTATTAATTTTATTA
 AGCAATCGATTTCAAACTTTTCCAAATTTCTCCAATCTCGAAATTAATTTACTGTGTCAGAAACAGAAATATCAC
 GCTTGTGTAAGAGTACCCCGCAGAGTTATGCAAAATAGTCTCTTTTCAAGCTCATATCCGGAACGACCGCTCAA
 CAGATTTAGAGTTTGACCCACCTGGAATTTTATCATTTTCAACCGTCTCTTAAATAAGGCCAATGTGCTGCTT
 ATGGAAGAAAGCTTAGATTAAAGCTCAACAGTATTTTCTTATTGGGCAACCAATTTGTAATAATCTTCTGCA
 TTGCTGTTTAAATCTGTCTGCAAAATAGCAATGCTCAAGTGTAAAGTGAACATGAAATTTTCAAGCAATCTCTCATG
 TCAAAATTTTAGATTGTGACCAAAATAGACTAGACTTTGATAAGTGTAGTGTCTTACTGAAATGTCCGACTTGG
 AAGTTCTAGATCTCAGCTATAATTTACACATTTTCAAGATAGCAGGCGTAAACATCATCATPAGAATTTATTCAAA
 ATTTTCAACAATCTAAAAAGTTTAAACTTGAGCCACAAACAACTTATACTTTAAACAGATAAGTATAAACCCTGAAA
 GCAAGTCCCTGGTAGAATTAGTTTTCAGTGGCAATCGCTTGACATTTTGTGGATAGTGATGACAAACAGGTATA
 TCTCCATTTTCAAGGCTCTCAAGAACTGACAGCTCGGATTATCCCTTAATAGATGATGACACATCCCAAACT
 AAGCAATCCCTTAATTTGCGACGAGTCTCACTGAATACATATAAATGATAATATGTTAAAGTTTTTTAACTCGA
 CATTTACTCAGCAGTTCTCCTGCTCGAGTTGCTTGACTTACGTGGAAACAACTACTCTTTTAACTGATAGCC
 TATCTGACTTTACATCTCCCTTCGGACACTGCTGCTGAGTCAATAACAGGATTTCCCACTACCCCTCTGGCTTTC
 TTTCTGAAGTCAGTAGTCTGAAGCACTCGAATTTAAGTTTCAATCTGCTGAAAAACAACTACAAATCCGCACTTG
 AAACATAGACCAACCAAAATTTATCTATGTTGGAACTACACGGAACCCCTTTGAATGCACTGTGACATTTGGAG
 ATTTCCGAAGATGGATGGATGAACATCTGAATGTCAAAATTTCCAGACTGGTAGATGTCAATTTGTGCGAGTCTGT
 GGGATCAAAAGAGGGAAGATATTGTGAGTCTGGAGCTAACAACTTGTGTTTCAAGTGTCACTGCAGTGATATTAT
 TTTTCTTCAAGTTCTTTATCACCACCATGTTATGTTGGCTGCCCTGGCTCAACATTTGTTTACTGGGATGTTT
 GGTTTATATATAATGTGTGTTTAGCTAAGGTAAAAGGCTACAGGTCTTTTCCACATCCCAAACTTTCTATGATG
 CTTAATTTCTATGACACCAAAGATGCTCTGTTACTGACTGGGTGATAAATGAGTGTGCTTACCCTTGAAG
 AGAGCCGAGACAAAAACGTTCTCCTTTGTCTAGAGGAGAGGATTTGGACCCGGGATTTGGCCATCATCGAACCC
 TCATCGAGACGATCAACCAAGAGCAAGAAAAAGTATTTGTTTAAACCAAAAAATGCAAAAAGCTGGAACTTTA
 AAACAGCTTTTACTTTGGCTTTGAGAGGCTAATGGATGAGAACTGGATTTGATTTATTTACTCTGCTGGAGC
 CAGTGTCTACAGCATCTCAGTATTGAGGCTACGGCAGCGGATCTGAAGAGCTCCATCTCCAGTGGCCGTGACA
 ACCGAGAGGCGAGAGGCTGTTTGGCAAACTCTGAGAAATGTGCTTCAAGTGAATTTTAAACAAACACA
 ATATGATGTGCAATTCATTAAGCAATACTAACTGACGTTAAGTCATGATTTCGCGCCATTAATAAGATGCAAG
 GAATGACATTTCTGATTTAGTTATTTGCTATGTAAACAAATTTCCCAAACTTAGTGGTTTAAACAAACACA
 TTTGCTGCGCCACAGTTTGTGAGGTCAGAGTCCAGGCCACGATCAATCGGGTCTCTGCTCAGGGTGTCTAG
 AGGCTGCACTTGAAGTGTTCACAGAGACATAGGCATCACTGGGTCACATCTCATGTGGTTGTTTCTGATTTCA
 ATTCTCTCTGGGCTATTGGCCAAAGGCTATACTCATGTAAGCCATGCGAGCTCTCCCAACAGGCGAGTGTCTTC
 ATCAGAGCTGACAAAAAGAGAGGTTGCTAGCAAGATGAAGTCAAACTTTTGAATCGAATCAAAAAGAGTAT
 ATCTCATGTTTGGCCATTTCTATTGTTAGAAAGTAAACACAGTCCCAACAGTCCATGGAAGTGAACAC
 TCAGTCCAGGAAAACAGCTGAAGACCAAGATGGTGAAGTCTGATGCTTGAAGTGTGATCAACTATTTTCCCT
 TGACTGTGCTGGGATGGCTGCTATCTTGATGATAGATTGTGAATATCAGGAGGCGAGGATGACCTGTTGAAC
 ATCTTAGCAGTTGACCTAACACATCTCTTTTCAATCTAAGAACTTTTGCCACTGTGATGCTGTTGCTGCTAAT
 TTAAGCTGTGTTTATATTATATATATCTATGGCTACATGGTTATATTGCTGTGGTGGCTGGGTTTAT
 TTAACGTTGCTTTTCAAAATTTGCTGTAACATTTTGACTCTTAAGGTTAGATGCAATTAAGAACTAGATGG
 ATAGCTTTTAAAGCATCTTTTACTCTTACCATTTTTAAAGATGATGAGCTTAAATTCGAAGCTTTTGGTCTATA
 TTGTTAATTGCCATTGCTGTAATCTTAAATGAATGAATAAAATGTTTCAATTTTACAAAAA

FIGURE 211

MENMFLQSSMLTCIFLLISGSCELCAEENFSRSYPCDEKKQNDSVIAECSNRRLQEVPTVG
KYVTELDLSDNFITHITNESFQGLQNLTKINLNHNPNVQHONGNPGIQSNGLNITDGAFLNL
KNLRELLLEDNQLPQIPSGLPESLTELSLIQNNIYNITKEGISRLINLKNLYLAWNCYFNKV
CEKTNIEDGVFETLTNLELLSLSFNSLSHVPPKLPSSLRKLFSLNTQIKYISEEDFKGLINL
TLLDLSGNCPRCFNAPPCVPCDGGASINIDRFQNLTLQRLYNLSSTSLRKINAAWFKNM
PHLKVLDELFNYLVEIVSGAFLTMLPRLEILDLSFNFIKGSYPQHINISRNFSKLLSLRAL
HLRGYVFQELREDDFQPLMQPLNLTINLGINFIKQIDFKLFQNFSLNLEIYLSNRISPLV
KDRQSYANSSSFQRHIRKRRSTDFEFDPHSNFYHFTRPLIKPQCAAYGKALDLSLNSIFFI
GPNQFENLPDIACLNLANSNAQVLSGTEFSAIPHVKYLDLTNNRLDFDNASALTELSDELV
LDLSYNSHYFRIAGVTHHLEFIQNFTNLKVLNLSHNNIYTLTDKYNLESKSLVELVFSGNRL
DILWNDDNRYISIFKGLKNLTRLDLSLNLKHIPNEAFLNLPASLTEHLHINDNMLKFFNWT
LLQQFFRLELLDLRGNKLLFLTDSLSDFTSSSLRTLLLSHNRI SHLPSGFLSEVSSLKHL DLS
SNLLKTINKSALETKTTTKLSMLELHGNPFECTCDIGDFRRWMD EHLNVKIPRLVDVICASP
GDQRGKSIVSLELTTCVSDVTAVILFFFTFFITTMVLAALAHHLFYWDVWFIYNVCLAKVK
GYRSLSTSQTIFYDAYISYDTKASVTDWVINELRYHLEESRDKNVLLCLEERDWDPLAIIID
NLMQSIQSKKTIVFVLTKKYAKSWNFKTAFYLALQRLMDENMDVIIFILLEPVLQHSQYLRL
RQRICKSSILQWPDNPKAEGLFWQTLRNVVLTENDSRYNMYVDSIKQY

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 826-848

00978664-101601

FIGURE 212

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCTCCCGGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCAOGGCTGCAAGGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCTGAGGCCCCAGC
AAGGGCTAGGGTCCATCTCCAGTCCAGGACACAGCAGCGGCCACCATGGCCACGCTGGGC
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGAGGA
GCAGCTCCTGCCCCGTGTCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAA
GGCCACCCCGCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTT
CTGGTGTGTGGCAGTGGGCGGCACAGAGCACGCTACCGGCCCGGCTAGGGTGTGTGCTGT
CCGGGCTCAGCGGGACCTGTCTCCGAGTCTGTCGTCAGCGTGTGTACCAGCCCTTCCTCA
CCACCTGCGACGGGACCGGGCTGCGACCTACCGAACCATCTATAGGACCGCCTACCGC
CGCAGCCCTGGGCTGGCCCCCTGCCAGGCCCTCGCTACGCGTGTGCCCCGGCTGGAAGAGGAC
CAGCGGGCTTCTGGGGCTGTGGAGCAGCAATATGCCAGCGCCATGCCGAACGGAGGGA
GCTGTGTCCAGCCTGGCCGTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCA
GATGTGGATGAATGCAGTGTAGGAGGGGCGGCTGTCCCAGCGCTGCATCAACACCGCCGG
CAGTTACTGTGTCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGC
CCAAGGGAGGGCCCCCAGGGTGGCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAA
GAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGTGGAGGAGAAGCTGCAGCTGGTGTGGC
CCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCC
TGGTGCACTCCTTCCAGCAGCTCGGCGCATCGACTCCCTGAGCGAGCAGATTTCCTTCCTG
GAGGAGCAGCTGGGGTCTGTCTCCTGCAAGAAAGACTCGTGAAGTCCCCAGCGCCCCAGGCTG
GACTGAGCCCCCTCAGCGCCCTGCGAGCCCCCATGCCCTGCCCAACATGCTGGGGGTCCAG
AAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTTCTCCTCCTCCC
TTCCTCGGAGGCTCCCAGACCTTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCAC
CCCTGGCTACCCCAACCTTGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCCCAGCTG
AGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGACCATGGCACAGGCCAGGCAGCCCCGAG
GCTGGGTGGGGCTCAGTGGGGGCTGCTGCCCTGACCCCGACACAATAAAATGAAACGTGA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCGCGACTTAGAGT
CGACCTGCAGAAGCTTGGCCGCATGGCCAACTGTTTATTGCAGCTTATAATGGTTACAAAT

FIGURE 213

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLADGTL CVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

09978564-101601

FIGURE 214

GCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAG
GGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCC
AGCAGCATCAGAGCAGCCCCGTGTGGTTGGCAGCAAAGTTTCTAGCTTGGCTGGGCCCGCTGTGA
GGGGCTTCGCGCTACGCCCTGCGGTGTCCCGAGGGCTGAGGTCTCCTCATCTTCTCCCTAGC
AGTGGATGAGCAACCAAACGGGGGCCGGGGAGGGGAATGGCCCCGAGGAGAGGAAACCC
AAAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATCCAGGCAGCCCCCAGGACCGGGGAGG
CACAGGTGGCCCCACCAACCGGAGGAGCAGCTCCTGCCCTGTCCGGGGGATGACTGATTTC
TCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGCTGGAGGCACAGGCCATGAGGGGC
TCTCAGGAGGTGCTGTGATGTGGCTTCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTA
CCGGCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACGGGGACCCCTGTCTCCGAGTCGTTCC
TGCAGCGTGTGTACCAGCCCTTCTCTACCACCTGCGACGGGCACCGGGCCTGCAGCACCTAC
CGAACCATCTATAGGACGCGCTACCGCCGAGCCCTGGGCTGGCCCTGCCAGGCCTCGCTA
CGCGTGTCTGCCCGGCTGGAAGAGGACCAGCGGGCTTCTGGGGCCTGTGGAGCAGCAATAT
GCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCA
GGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGTCTAGGAGGGGCGGCTG
TCCCCAGCGTGCATCAACACCGCCGGCAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCC
TGTCTGCAGACGGTACACTCTGTGTGCCCCAAGGGAGGGCCCCCAGGGTGGCCCCAACCCG
ACAGGAGTGGACAGTGCATGAAGGAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGTCT
GGAGGAGAAGCTGCAGCTGGTGTCTGGCCCCACTGCACAGCCTGGCCTGCGAGGCACTGGAGC
ATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACCTCTTCCAGCAGCTCGGCCGATCGAC
TCCTTGAGCGAGCAGATTTCTTCTCTGGAGGAGCAGCTGGGGTCTGCTCTCTGCAAGAAAGA
CTCGTGACTGCCAGCGCTCCAGGCTGGACTGAGCCCCCTACGCCGCCCTGCAGCCCCCATG
CCCCTGCCAAATAGCTGGGGGTCCAGAACCCACCTCGGGGTGACTGAGCGGAAGGCCAGGC
AGGGCCTTCTCTCTTCTCTCTCTCTCGGGAGGCTCCCAGACCTTGGCATGGGAT
GGCTGGGATCTTCTCTGTGAATCCAACCCCTGGCTACCCCCACCTGGCTACCCCAACGGCA
TCCAAAGGCCAGGTGGACCCCTCAGCTGAGGGAAGGTACAGAGCTCCCTGCTGGAGCCTGGGAC
CCATGGCACAGGCCAGGCAGCCCGAGGCTGGGTGGGGCCTCAGTGGGGCTGTGCTGCTGAC
CCCCAGCACATAAAATGAAACGTG

09378564.101501

FIGURE 215

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLADGTLCVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

109101-1958/660

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CCACACGCTCCGAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGACAGGCCAGGCA
GGTGGGCTCAGGAGGTGCTCCAGGCGGCCAGTGGGCTTGAGGCCACAGCAAGGGCTAGGG
TCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATTGGCCACGCTGGGCTCCAGCAGCAT
CAGCAGCCCCCAGGACCGGGGAGGCACAGTGGCCCCCACCACCCGAGGAGCAGTCTCTGC
CCCTGTCCGGGGGATGACTGATTCTCTCTCCGCCAGGCCACCAGAGGAGAAGGCCACCCGC
CTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGC
AGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACG
GGGACCTGTCTCCGAGTCTGTCTGTCAGCGTGTGTACAGCCCTTCTCTACCACCTGCGAC
GGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGG
CTGGCCCCCTGCCAGGCCCTCGCTACGCCGTGCTGCCCCGGCTGGAAGAGGACAGCGGGCTTC
CTGGGGCCTGTGGAGCACAATATCGCAGCGCCATGCGGAAGCGAGGAGCAGTGTGCTCCAG
CCTGGCGCTGCGCTGCCCCTGCAGGATGGCGGGTGACATCGGAGCTCAGATGTGGATGA
ATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCGTGTCAACCCGCCGCAGTTACTGGT
GCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCAAGGAGGG
CCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGAATGAAGGAAGAATGCAGAG
GCTGCAGTCCAGGTTGACCTGCTGGAGGAGAAGCTGCAGCTGGTGTGCTGGCCCCACTGCACA
GCCTGGCTCGCAGGCACTGGAGCATGGGCTCCCGACCCCGGCAGCCTCTGGTGCACCTC
TTCAGCAGCTCGGCCGATCGACTCCCTGAGCGAGCAGATTCTCTTCTCTGGAGGAGCAGCT
GGGTCCTGCTCCTGCAAGAAAGACTCGTGACTGCCACGCGCCCGAGGCTGGACTGAGCCCC
TCACGCCGCCCTGCAGCCCCCATGCCCCCTGCCCAACATGTCTGGGGGTCCAGAAGCCA CCTCG
GGGTGACTGAGCGGAAGGCCAGGCAGGGGCCCTTCTCTCTTCTCTCTCTCCCTTCTCTCGGAG
GCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACC
CCCACCTTGGCTACCCCACCGGCACCTCAAGGCACAGGTGGGCCCTCAGCTGAGGGAAGGTAC
CAGTCTCCTGTGGAGCTGGGATCCCATGGGCACAGGCAGGCCAGCCCGAGGCTGGTGGGG
CCTCAGTGGGGGCTGCTGCTGACCCCGACGCAAAATAAATGAACGTG

FIGURE 217

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCSDVDECSARRGGCPQRCVNTAGSYWCQCWEGHSLSADGTLCVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

0997564-11101
109111-1498/650

FIGURE 218

GGTTGCCACAGCTGGTTTAGGGCCCCGACCACTGGGGCCCCCTTGTCCAGGAGGAGACAGCCTCCCGGCCCGGGGAG
GACAAGTFCGCTGCCACCTTTGGCTGCCGACGTGATTCCCTGGGAGCGTCCCTTTCTCCGCGCTCAGCTGCCGCGG
AGTTGGGTCTCCGCTGTTTCAGGCCCGGCTCCGCCCTTCCTGGTCTCCCTTCTCCCGCTGGGCCGGTTTATCGGGAGG
AGATTGTCTTCAGGGCTAGCAATTGGAATTTTGATGATGTTTGACCCAGCGCGCAGGAATAGCAGGCAACGTGAT
TTCAAAGCTGGGCTCAGCCTCTGTGTTCTTCTCTCCTGTAATCGCAAAACCCATTTTGGAGCAGGAATTCGAATCA
TGTCTGTGATGCTGGTGAGAAAGAGGTGACACGGAATGGGAGAACTCCAGGCAGGAACAACCTTTTGTCTGTG
ATGCGCCCGCTCATGATGGCCCGGCAAAAGGGCATTTTCTACCTGACCCCTTTTCTCTCATCTCGGGGACATGTACAC
TCTTCTTCGCCCTTGTAGTGCCGCTACCTGGCTGTTCAGCTGTCTCCTGCCATCCCTGTATTGTCTGCCATGCTCT
TCCTTTTCTCCATGGCTACACTGTTGAGGACAGCTTCAGTGACCTGGAGTGATTCTCGGGCGCTACCAGATG
AAGCAGCTTTTATAGAAATGGAGATAGAAGCTACCAATGGTGGGTGCGGCCAGGGCCAGCGACACCGCCTCGTA
TCRAGAATTTCCAGATAAACCAACAGATTGTGAAACTGAAATACTGTTACACATGCAAGATCTTCGGGCCCTCCCC
GGGCCTCCCATTTGCAGCATCTGTGACAACTGTGTGGAGCGCTTCGACCATCACTGCCCTCGGTGGGGGAATTGTG
TTGGAAAGAGGAACCTACCGCTACTTCTACCTCTTCATCCTTTCTCTCTCCCTCCTCACAATCTATGTCTTCGCT
TCAACATCGTCTATGTGGCCCTCAAATCTTTGAAATTTGGCTTCTTGGAGACATTTGAAAGAACTCCTGGAAGT
TTCAGAACTCCTCATTGCTTCTTTACACTCTGGTCCGTGGTGGGACTGACTGGATTTTCACTTTTCTCTGGG
CTCTCAACCAGACAACCAATGAAGACATCAAGGATCATGGACAGGGAAGAATCGCGTCCAGAATCCCTACAGCC
ATGGCAATATTGTGAAGAACTGCTGTGAAGTGCTGTGTGGCCCTTGGCCCGAGTGTGCTGGATCGAAGGGGTA
TTTTGCCACTGGAGGAAAGTGGAGTGCACCTCCAGTACTCAAGAGACCAAGTACAGCCTCTTGGCCACAGAGCC
CAGCCCCACAGAACCTGAACTCAAATGAGATGCCGAGGACAGCAGCACTCCCGAAGAGATGCCACCTCCAG
AGCCCCCAGAGCCACACAGGAGGCAGCTGAGAGTGTGAGAAGTACGCTATCTATGGAAGAGACTTTTGTGTTGT
TAATTAGGCTATGAGAGATTTTCAAGTGTGAGAAGTTAAACCTGAGACAGAGAGCAAGTAAAGCTGTCCCTTTAACT
GTTTTCTTGGTCTTTAGTCAACCCAGTGTGCACACTGGCATTTTCTGCTGCAGACTTTTAAATTTCTGAAT
CAAGGCAGTGGCAGAAGATGTGAGTCACTCTGATAACTGGAAAAATGGGTCTCTTGGCCCTGSCACTGGTTCT
CCATGGCTCAGCCACAGGGTCCCCCTGGACCCCTCTCTCCCTCCAGATGCCAGCCCTCTGCTTGGGGTCA
TGCTCTCATTTGGGGCTAAAGTTTGTGAGACTGGCTCAAATCTCCCAAGCTGCTGCAGTGTGAGTCCAGA
GGCAGTCAAGAGACTCTGGCCAGGGGATCTCAACTGGGTCTTGGGGTCTTCAGGACTGAAGAGGGGGAGAG
TGGGTGAGAAGATTCTCTCGGCCCAACCAAGTCCAGCATTCGCCCAAAATCCTTTTAGGAATGGGACAGGTACCT
TCCACTGTGTATANN
CAGGAATGCCAGTAATAAAGTCTGCACTTTGGTCACTTTCTTCTTCTCAGAGGAAGCCGAGTGCTCACTTAAAC
ACTATCCCTCAGACTCCCTGTGTGAGGCCCTGCAGAGGCCCTGAAATGCACAAATGGGAAACCAAGGCACAGAG
GCTCTCTCTCTCTCTCTCTCCCGATGTACCTCAAAAAAATAAATGCTAACAGTTCTTCCATTAAAGCT
CGCTCAGTGAAGGAAAGCCAGCATGCTGCCCTCTCGGGTAACCTCAACCTAAGGCTCGGGCCACCTCTGGCT
ATGTAACCAACTGGGGCTTCTTCCAGCCCGCTCTTCCAGCACTTCCACCGGCAGAGTCCACAGGCCACTT
CACCTTGGGCTGTGGCCCGCAGTCAGCTCTGCTCAGGACTGCTCTATTTCAGGGAAGAGATTATGT
ATTATATGGCTATATTTCTTAGAGCACTGTGTTTCTCTTTTCAAGCAGGGTCTGCTGCTGAGTACTAT
CGGTGGGGAGTGAACCCGAACCTTTTCACTTATTGAAGGCGATTAACTGTGCTCATATGCA

0973564-101601

FIGURE 219

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGIFYLTFLILGTCTLFFAFECRYLAV
QLSPAIPVFAMLFLLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPP
RIKNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHHC PWVGN CVGKRNYRYFYL
FILSLSLLTIIYVFAFNIVYVALKSLKIGFLET LKETPGTVLEVLI CFFT LWSVVGLTGPHTF
LVALNQTTNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVL CGPLPPSVLDRRGILPLEESGSR
PPSTQETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPPEPPEPPQEAAEA EK

Putative transmembrane domains:

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245

FIGURE 220

AAAACCCCTGTATTTTTTACAATGCAAATAGACAATNANCCCTGGAGGTCTTTGAATTAGGTAT
TATAGGGATGGTGGGGTTGATTTTINTTCCTGGAGGCTTTTGGCTTTGGACTCTCNCTTTCT
CCCACAGAGCNCTTCGACCATCACTGCCCCTGGGTGGGGAATTGTGTTGGAAAGAGGAAC TA
CCGCTANTTCTACCTCTTCATCCTTTNTCTCTCCNCCTCACAATCTATGTCTTCGCCTTCA
ACATCGT

109101-4958/660

FIGURE 221

GTGTGTCTCTCAGCAAAAAGTGGATTTAAATCTCTTGCAAGCTTGAGAGCAACACAA
TCTATCAGGAAAAGAAAAGAAAAAACCGAACCTGACAAAAAGAGAAAAGAGA
AAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATT
GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGA
CAAGTGGTGCTGGATCTCGCGTGGTCTTCTGAGCAACACCCAAACGCAGTACAGCATCG
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCGAGACAGACAAC
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTTAGAGAGATTTC
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGAC
GAATACTTTGGAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCCTC
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAGTATCCACCATACA
TTTCAGAAGCCAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC
TCAGCAGTCCCTCAGCAGAATTCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA
GAAAGGGGTGAAAGTGAAAAACAGACCTTTCCTCTCAAACTCATCTTCTTCAATGTCTCTG
AACATGACTATGGGAACACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC
ATCATGCTATTTGGTCCAGGCGCCGTGAGCGAGGTGAGCAACGGCAGCTCGAGGAGGGCAGG
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACTGCTTCTCAAATTTGATGTGAGTGCC
ACTTCCCCACCGGGAAAGGCTGCCGCCACCACCACCAACACAACAGCAATGGCAACAC
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGAAAAGAGTTTAAAAAAGAAATGAA
AATTGCCCTTGCAATATTTAGGTACAATGGAGTTTCTTTTCCCAAACGGGAAGAACACAGC
ACACCCGGCTTGAGCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA
GGGCTCAGCCTCTCTGCCACAGAGTGCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA
AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGCCCAAGCGTGCGCTGCGG
GCACCTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA
AAAAA

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FIGURE 222

MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFFPKAMDNVTVRQGESATLRCTIDNR
VTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDDVYDEGPYTCVQTDNHPK
TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTVRHHISPKAVGFVSEDEYL
EIQGITREQSGDYECASNDVAAPVVRVKVTVNYPPIYSEAKGTGVPVGQKGTLCQCEASAV
PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNVTCVASNKLGHNTNASIML
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLKKF

Signal peptide:

amino acids 1-28

109104-453760

Copy to: John J.

GAAAAAAATCATGAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTTGGGCAATCTTC
 ACGGGGCTGGTCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGACGCGAGATGCCACCTT
 CCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCATA
 TTGACAACCGGGTCACCCGGGTGGCTTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAAT
 GACAAGTGGTGCTGGATCCTCGCGTGGTCTTCTTGAGCAACACCCAAACGCAGTACAGCAT
 CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACA
 ACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCAAAATTGTAGAGATT
 TCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAG
 ACCAGAG

FIGURE 224

ATGGCTGTTGACGGCGGGGCCGGGACCGGGGCCGGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGA
ATACCCGCTCGGCCGACTCCACCATGGAACGTCGCGCTGCAGGAGCTGGGAGCTGGGAGCTGGGAGCAACGTTGGGATTTCAG
AAGGGGACAAGACAGCTGTTAGGCTCACGACCGAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTACTGCTGGCT
GCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCAGTACCAAGAGACCCATCCACAGCACCTGCCTTACA
GAGGCTCGCATTCGATGGCTGGAAAAATCTGGAGTTCCTGGACCGAGGGGTGAGCCCTGTGAGGACTTTTAC
CAGTTCTCTGTGGGGCTGGATTTCGGAGGAACCCCTGCCCGATGGGGCTTCTCGCTGGAACACTTCTAACAGC
CTCTGGGACCAAAACAGGCCATACTGAAGCACCTGCTTGAAGAACACCACTTCACTCCAGCAGTGAAGCTGAG
CAGAAGACACAGCGCTTCTACCTATCTTGCTACAGGTGGAGCGCATTGAGGAGCTGGGAGGCCAGCCACTGAGA
GACCTCATTTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACAGGACAACCTTATGAGGTTTGAAG
GCACTAGCAGGGACCTACAGGGCCACCCCATTTCTCACCGCTCTACATCAGTCCGCACTTAAAGATTCCAAACAGC
AATGTTATCCAGGTGGACAGCTCTGGGCTCTTCTGCCCTCTCGGGATTACTACTTAAACAGAAGTGCCTAATGAG
AAGGTGCTCACTGCCTATCTGGATTACATGGAGGAAGTGGGGATGCTGCTGGGTGGGGCCCACTCCACGAGG
GAGCAGATGCAGCAGTGTCTGGAGTTGGAGATACAGCTGGCCAAACATCACAGTGCCTCCAGGACAGCGGCGGAC
GAGGAGAAGATCTACCAAAAGTAGCATTTCGGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAATTC
CTGTCTTTCTGTCTGCACATTGGAGTTGAGTGACTCTGAGCCTGTGGTGGTGTATGGGATGGATTATTTGCAG
CAGGTTGCAGAGCTCATCAACCGCACGGAACCAAGCATCCTGAACAAATTAACCTGATCTGGAACCTTGGTGCACAAAG
ACAACCTCAAGCGCTGGACCGACCTTTGAGTCTGCACAGAGAAGCTGTGGAGACCTCTATGGCATTAAGAAG
TCTCTGTGCGCGAGGTGGCAGACCTGCATCTCAACACGAGATACGCGCTTGGCTTTTGGGGTCACTCTTC
GTGAGAGCCCACTTTGACCGGCAAGCAAGAAATTCAGAGGGGATGATCAGCGAAATCCGACCGCATTTGAG
GAGGCGCTGGGACAGCTGGTTTGGATGGATGAGAAGACCGCCAGGAGCCAGGAGAAGCAGATGCCATCTAT
GATATGATTGGTTTCCAGACTTTATCTGGAGCCCAAGAGCTGAGTGAATTTATGACCGGTACGAATTTCT
GAAGATTCTTTCTCCAAACATGTTGAATTGTACAACCTTCTTGCCAAAGTTATGGCTGACCAAGCTCCGCAAG
CCTCCACGCGGAGACAGTGGAGCATGACCCCCAGACAGTGAATGCCTACTCTTCAACTAAGATGAGATC
GTCTTCCCCGCTGGCATCTCTGAGGCCCCCTCTATGCCCGCAACCAACCCAGGCGCTTGAACCTTCGGTGGCATC
GGTGTGGTCTATGGGCCATGAGTTGACGCATGCTTTGATGACCAAGGGCGCAGTATGACAAAGAGGGGACCTG
CGGCCCTGGTGGCAGAAAGTGTCTTGCAGCCTTCCGGAACCAACCGCTGCATGGAGGAACAGTACAATCAA
TACCAGGTCAATGGGGAGAGGCTCAACGGCCGCGCAGAGCTGGGGGAGAACTTACTGACAAACGGGGGCTGAAG
GCTGCTACAAATGCTTACAAGCATGGCTGAGAAAGCATGGGAGGAGCAGCAACTGCCAGCGCTGGGGCTCACC
AACCACAGCTCTTCTCTGTGGGATTGCCCCAGTGTGTGCTGCTGGGCACTCTCTCAACTCCCGTGACTCTCTGGG
CTGTTGACCGACCCCAACAGCCTGCCCGCTTCCGCTGTGCTGGGCACTCTCTCAACTCCCGTGACTCTCTGGG
CACTTCCGCTGCCCTGTCCGCTCCCCATGAACCCAGGGCAGCTGTGTGAGTGTGGTAGACCTGGATCAGGGGA
GAAATGGCCAGCTGTCAACAGCCTGGGGCAGCTCTCTGACAAAGCTGTTTGGCTCTTGGGTTGGGAGGAAGCAA
ATGCAAGCTGGCTGGCTAGTCCCTCCCCCAAGGTGACATGAGTACAGACCTCTCTCAATCAACCAATTG
TGCTCTGCTTTGGGGTGGCCCTGCTCCAGCAGAGCCCCACCATTCACTGTGACATCTTTCGGTGCACCT
GCTTGAAGAGGCTTGGGTGGGAGGCGAGTTCCATAGGAAGGAGTCTGGC

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FIGURE 226

GCCCGGCCCTCCGCCCTCCGCACTCCCGCCTCCCTCCCTCCGCGCGCCTCCCGCGCCCTCCCTCCCTCCCTCCCTCC
 CAGCTGTCCGTTTCGCTGTCAGCGCAGGCTCCCGGCCCGCGCGGCCCGCGCTGCTGCTCTCCGCGCTGCTGCTGCT
 CGGCTCCCGGCCCGCGCGCGCGCGCCAGAGCCCGCCCGTGTGCTGCCATCCGTTCTGAGAAAGGACCGCTGCC
 CGTTCTCGGAGAGCGGAGCTAGGTGGCGCCCGGGGAGCGCGGCGGGAGTCCGGCTCCGGGCGAGTTCAGCGC
 CACGCCGAGAGGGGCGCGGGGCGCAGGTGGCTCGCGCGCGCGCGCGCGGAGGCTGGGCGGGGCGCAGAGGAC
 GCGGTGCTTCGGGACCCCGGACCCGCGGGGCGAGCCCCCGGGGCGGACACCGGCGGAGCTGGGACAGCGGCTCCAGC
 CAGCGCTCCGCGCAGGAGCTCAGCTTCGGCGGGAGAGTCTATGCTTGGACGAGAGCTGGACCCCGGACCTTAGG
 GGAGCCATTCGGGCTGATGCGCTGCTGCTGCGCTCGGAGGCGCAGTGGGCTCGCGCTACCGAGGGCCCTCGG
 CAGGCTCAGTTCGAAAGAACCTCAAAACAGAGTGCACAAACCCGCGCTGTGGGACCGCGCGCGGAGCTGCGGAGCA
 CTGCTGCGCAGACCTCCGCCAGGACTTCGTGGCGCTGCTGACAGGGCGGAGGTTCGACAGGCGGTGGACAGGACCGG
 AGTCTCGCTGCTCGCCTTAGCCTTCGCTTCTCTATCTCTACAGGCGGTGGAGCGGCTCCAGGATTCGCTT
 CTCAGACTCCAAATGGCAGTGTCTGTTTGGAGCACCTGCAGCCCGACCCCAAGATGGCTGGTCTGTGGGGTGTG
 GCGGGCAGTGCCTCGGTTGTCTCTGCGGCTCCTTAGGGCGAGAACAGCTGCATGTGGCACTTGTGACACTCACTCA
 CCCTTCAGGGGAGGTTCGGGGGCTCTCATCCGGCACCGGGGCTGTCCCGAGAGACCTTCAGTGCATCTCTGAC
 TCTAGAGGCGCCCGACAGCAGGCGGCTAGGGGGCATCACCTGCTCACTTCAGTGACACAGAGGACTCCTTGCA
 TTTTGTGCTGCTCTCCGAGGCTTCAGGACTAAACCAAGTTCCTTCAGGCTCCAGATTCTACACCAAGGGGCA
 GCTACTGCGAGAACTTCAGGCCAATGTCTCAGCCAGGAACAGGCTTTGCTGAGGTGCTGCCCAACTGACACT
 CAGGAGATGGACTTGGCTGTGCTGGGGAGCTGCAGATGGCCCTGGAGTGGGCAAGCGGCGAGGGCTCGCAT
 CAGTGACACATTCGCTGCGCAGGAGAGCTGCGAGCTCCTGCAAGAGTTCCTTTGGGGCTTAAGTGCATGATGCC
 AGTCCAAACCGGGTGTGCGCGCTCAGCCAGGCTCACTTCGTAGGAAATGGCNCCTGATCCTCCAGGTGCAAT
 GGTAGGAGCAACAGTGGAGGTGGCGCATGACACTGGAAACCAAGCTCAGCGAGGCTCAGCCCACTGTGCTC
 GTGCCACATGGCTGGCTCTCTCCCTCGCCCCAGGCGCTGGGTATTCGCCCTGGGCTGGGCTGGCCAGGGGCG
 TCTATGTCTGCTGACGAATAGCTCTTCTGAAGCTGGGCAACAGGACTCCCAAGTGGAGAGCTTCGGGGGCA
 ACCTGGCTGCGCTCCCTCACTGCTGGGGCATAGCGCCCGCGCTGCGCGGTGCGCGCTAGCAGGAGCGCTTGTGTACC
 CTGTGTGAGAGAGCAAGACAGCAGGCGACGCTGGCTTTCTTTGGATACCCCTCAGGCTCATGTAGAGTGTCT
 GCTGGCTGGGCTTGTGGCTCAGAAACAGGCACTGTCACTGCCCACTCCTTTGGGCTCCTGGAAAGCGCAGGCG
 TCGCGGCTGCTGAGAGGCTTATAGGCTCAGGCTCAGGCGTGGTGAAGAGCTGGAGCGGGAAGCTTCGGGCG
 GCACCTGCGCAAAAGGCAATGGCTTCTCTGATGATCACCAACAGGTAGCCCGAGGCGGAGCTCGAGGGCAGGCT
 CTCTCCCAAGGTGACATAGCAACCAATGTGAGGTGTGGCGGACTGCGGCTGGAGGCGCGCGGCGGAGGGGT
 CGGGGCTGGGGGCTCCGGATACAGCTCTGTGTCGCGCCGCTGTGGTGCTGTGTCTCCCGGCCCTTAGCGCCCG
 CAAACCTGGTGCTCTGGGCGCGCCGAGAGCCCAACACATGCTTCTCGAGGCGCAGCAGCGCCCTCAGCGGCG
 TCGCTGGCGCCCACTACGACCCGCTCTGCTCACTTCGCACTTCGCAAGACCAAGCGTGATCTGTGAGCCGCT
 GGTGTGGCCACCCAGCTGCCACGCCACGCCGCTGCGAGGCTCCGACCAAGTGTGCTGCTTTCGCGGCTGCTA
 TTTTGTGTTGAGCGGAGCGGGGCGGGGCGGCTACGCGGTGGCAACCCCTTGTGGCCCGCTTTGGCTTAATTA
 GTGTGCTGTTCGACACTCGCAGCGGGGGGCGCTGGAGAGGTGCACTGTGAGAAAGTTCAGTGTCCCGCGCTGCT
 CTGTGCGCCAGCTGTGCGGTTCACCCCAACGACTGCTCAGAACAGTGTCCAGTGGAGGCCACCGCCGCTGAG
 GGAACCCATGCAGGCTGATGGGCGCCCGGCGCTGCGCTTTGCTGGGCACTGGTTCAGAGAGTTCAGAGCTGCTG
 CTGAGCTGAGTCCCGCTTTGGAGAGATGAGCTGTATCACTTCAGATGTGGGTAAGTGGGAGCAGGCACTTGT
 GTGAGTGGTCACTGGAGGCTGGCTTCGGATAGGAGACTTCCTCAGAGAGGCTGGAAGTCA
 CTGTGTCCTCACTGCTCTGCGGAGCACTCACTGTCTGTGCTTCGCTTCGTACCAAGGAGGGGTGCTCACTGTGAGC
 GAGTCACTGTTCACCTGCACTGTGCTGTGCTTCGCGGGAAGGAGAGTTCGATGCTGTTCCCGCTGCACGGCCACC
 GCGCGCTTAAGTGAAGGAGCTCAGGCTCAGCAGCTGTGAGTGGAGGGCTCACTGCTGCTGGGAGCTCTGATCAG
 GAAAGGAGCACTCACTGTGTGAGGAACAGTGCAGCTGCTCCTCACAAGTGCCATTCCAATCCACCTCAGCAGCA
 ACCTGGTGGAAATGTTATTTATGAGCTTTCTTTACAAATGAGATTCTGAAGCTCAGAGAAATTAAGCAACGAG
 ATGAGAGTCAACCCAGCTGTGTGCACTGACCTGTTTGAAGAAATAGTGGCTTCGAGGACAGGAGGAGGAGTGT
 TGGCTGCGCTCTATGCTCTCTGTGCTCTCACTCCCTCTCCCTCCCAACTTCCCTGAGCTTCTGTGCTGCTCC
 AGCAGCCCGAGAGCAGCAACTGATCCAGAGCTGGAGAAAGAGCGGAGGCTTCGTAGGAGAGCGGACGAGGGCG
 AAGTGACCAAGAGGATGGGGCTGAGCTGGGGAAGGGGTGGCATCGAGGACCTTCTTGGATTTCTCTGTGGGAAG
 CCAAGTGGCTTGTGCTCTGTGCTGCTCTATCTCCACCCCACTACCTCTGGGAAGCAAGCTCCACAGGGG
 GAGGAGCGCTGGGCGCAGCCAGGCTCAGCCACTCCAAGTCTCGCTGCGCACCTCGGCTCTGTCTGGGAA
 GCGCCCAACCTTTCTCTCTCATACATATGTCACTGGCTTGTGGGATTTTAAATTTATCTCACTCAGCAGCAAG
 GCGCCCGACCACTCACTCTGCTGCTGCCCTGAGCTGAGCAGAGTCAATTTGGAGAGTTCCTTGTATTTATTAAC
 ATTTCTTTTCACTCTTTGGGCACTGAGGTGGCTCTTGTGGCCAGGAACCTGAGTGGGGCTGGTGGAGAGGG
 CNGAGATAGGAGGTGAGAGAGAGGAGCTCAGCACTTGGGAGAGCTGAAGAGGCTGGAGAGGCGAGAGATAG
 CGTGGCCTTGGCTGGCATGCTGGGTTCCGACAGGGGCTGGGAGTGTTTGTGAGATGTGCTAGAGACTCAAG
 AATTTAGGAGAGTGAAGCAACCTTTGACTCAAGTTTAAAGTTTCCACATCGCTGCGCTGTTTGGTGACTTCAATG
 TTTGAAGTTGCTCCAGAGAGAGATCAAGGTGTCAACAGCCCTCTCTCCCTCCTTCCCTTCCCTTCCCTTCT

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FIGURE 227

GGCCGAGCGGGGTGCTGCGCGGCGGCCGTGATGGCTGGTGACGGCGGGGCCGGGCAGGGGA
CCGGGGCCGCGGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGAATCACCGCCTGGCCCGAC
TCCACCATGAACGCTCGCGCTGAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAGAAGGG
GACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTAC
TGCTGGCTGCACGTCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCA
TCCCACAGCACCTGCCTTACAGAGGCCCTGCATTGAGTGGCTGGAAAAATCCTGGAGTCCCT
GGACCGAGGGGTGAGCCCCTGTGAGGACTTTTACCAGTTCTCCTGTGGGGGCTGGATTTCGGA
GGAACCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGCCTCTGGGACCAAAAC
CAGGCCATACTGAAGCACCTGCTTGAAACACCACCTTCAACTCCAGCAGTGAAGCTGAGCA
GAAGACACAGCGCTTCTACCTATCTTGCCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCC
AGCCACTGAGAGACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAG
GACAACTTTATGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCATTCTTCAC
CGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGCAATGTTATCCAGGTGGACCAGTCTG
GGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAGAAAGTAAGGAAC
ATCTTCCGAACCCCCATCCCTACCCCTGGCTGAGCTGGGCTGATCCCTGTTGACTTTTCCTT
TTGCCAAGGGTCAGAGCAGGAAGGTGAGCCTATCCTGTACCTAGTGAACAAACTGCCCTT
CCTTCTTTCTTCTTTCTTCTCCTCCCTCCCTCCCTTCTTCCCTTTTCTTCTTCTTCTTCC
TCTTATTCTTCTAGTAGGTTTCATAGACACCTACTGTGTGCCAGGTCCAGTGGGGGAATTG
GAGATATAAGTTTCCGAGCCATTGCCACAGGAAGCGTTTCAGTGTGCATGGGTTTCATGGACCT
AGATAGGCTGATAACAAAGCTCACAAGAGGGTCTCTGAGGATTGAGGAGAGACTTATGGAGCC
AGCAAAGTCTTCTGAAGAGATTGCATTTGAGCCAGGTCTCTGTAG

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FIGURE 228

ATGCCTACTACCTTCCAATAAGAATGAGATCGTCTTCCCCGCTGGCATCCTGCAGGCCCCC
TTCTATGCCCCGCAACCACCCCAAGGCCCTGAACTTCGGTGGCATCGGTGTGGTCATGGGCCA
TGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACTGCGGC
CCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCACACGGCCTGCATGGAGGAACAG
TACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACAT
TGCTGACAACGGGGGGCTGAAGGCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATG
GGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACCAACCACCAGCTCTTCTTCGTGGGATTT
GCCCAGGTGTGTGTCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGGCTGGTGACCGACCC
CCACAGCCCTGCCCGCTTCCGCGTGTGGGCACTCTCTCAAACCTCCCGTGACTTCTTGCGGC
ACTTCGGCTGCCCTGTGGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACC
TGGATCAGGGGAGAAATGGCCAGCTGTCAACAGACCTGGGGCAGCTCTCCTGACAAAGCTGT
TTGCTCTTGGGTTGGGAGGAAGCAAATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCCACA
GGTGACATGAGTACAGACCCTCCTCAATCACCACATTTGTGCCTCTGCTTTGGGGGTGCCCT
GCCTCCAGCAGAGCCCCACCATTCACTGTGACATCTTTCGTGTACCCCTGCCTGGAAGAG
GTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGCTGCCTCTTCTGTCCCAGGCTCACT
CAGCCTGGCGGCATGGGGCTGCGGTGCCTGCCCCACTGTGACCCACAGGCCTGGGTGGTG
TACCTCCTGGACTTCTCCCCAGGCTCACTCAGTGCACCTTAGGGGTGGACTCAGCTCTGTC
TGGCTCACCTCAGGGCTACCCCCACCTCACCTGTGCTCCTTGTGCCACTGCTCCCACTG
CTGCTGTGACCTTCACTGACAGCTCCTAGTGAAGCCCAAGGGCCTCTGAAGGCCTCCTGC
TGCCCACTGTTTCCCTGGGCTGAGAGGGGAAGTGCATATGTGTAGCGGTAAGTGGTTCCCTG
GTCTTAGGGCACAAGCCTTAGCAAATGATTGATTCTCCCTGGACAAGCAGGAAAGCAGATA
GAGCAGGGAAGGAAGAACAGAGTTTATTTTACAGAAAAGAGGGTGGGAGGGTGTGGTCT
TGGCCCTTATAGGACC

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FIGURE 229

CCCACGCGTCCGAGCGCCGCCGAGAATTAGACACACTCCGGACGCGGCCAAAAAGCAACCGAGA
 GGAGGGGAGGCAAAAAACCGAAAAACAAAAGAGAGAAAAACACCCCACTAGCTGGGGTGG
 GGGGAAGAAAAGAAAAGAAAACCCACCCCAACCAAAAAAATAAAAAA
 AAAAAAATAAATCCTGTGGCGCGCCGCTGGTTCCCGGGAAGACTCGCCAGCACCCAGGGG
 TGGGGGAGTGCGAGCTGAAAGCTGCTGGAGAGTGAGCAGCCCTAGCAGGGATGGACATGATG
 TTCTTGGTGCGAGGGTGCTTGTGCTCGAACCACTGGCTGGCGGCTGCTCCTCAGCCTGTG
 CTGCCTGTCTACCTCTCTGCCTCCCGGCTGGACAGAGTGTGGACTTCCCTCGGGCGGCCGTG
 ACAACATGATGGTCAGAAAAGGGGACACGGCGGTGCTTAGGTGTTATTGGAAGATGGAGCT
 TCAAAGGGTGCTTGGCTGAACCGGTCAAGTATTATTTTTCGGGAGGTGATAAGTGGTCAGT
 GGATCCTCGAGTTTCAATTTCAACATTGAATAAAGGGGACTACAGCCTCCAGATACAGAATG
 TAGATGTGACAGATGATGGCCATACACGTGTTCTGTTACAGATCAACATACACCCAGAACA
 ATGCAAGTGCATCTAACTGTGCAAGTTCCTCCTAAGATATATGACATCTCAAATGATATGAC
 CGTCAATGAAGGAACCAACGTCACTCTTACTTGTGTGGCCACTGGGAAACAGAGCCTTCCA
 TTCTTGGCGACACATCTCCCCATCAGCAAAACCATTTGAAATGGACAATATTGGACATT
 TATGGAATTAACAAGGACAGGCTGGGGAATATGAATCAGTGCAGGAAAATGCTGTGTCTATT
 CCCAGATGTGAGGAAGTAAAGTTGTTGCTCACTTTGCTCCTACTATTTCAGGAAATTAAT
 CTGGCACCGTGACCCCCGGACGCGAGTGGCTGATAAGATGTGAAGGTGAGGTGTGCGCCCT
 CCAAGCTTTGAAATGGTACAAGGAGAGAGAAGAGCTCTTCAATGGCCCAACAAGGAATTTATT
 TCAAAATTTTAGACAAGATFCCATTCTCACTGTTACCAACGTGACACAGGAGCATCTCGGCA
 ATTATACCTGTGTGGCTGCGCAACAAGCTAGGCACAACCAATGCGAGCCTGCGCTCTTAACCT
 CCAAGTACAGCCAGTATGGAATTAACGGGAGCGCTGATGTTCTTTTCTCCTGCTGGTACCT
 TGTGTTTGACATCTCCTCTTACCAGCATATTCTACCTGAAGATGGCATTCTACAATAAA
 TTCAAGACCTTAATAAGGCTTTTAAGGATCTCTGAAAGTCTGATGGCTGGATCCAATCT
 GGTGATCTTGTAAAGCGCGTGGGATATAATCAGCAGTGTCTTACATGGGATGATCGCC
 TTCTGTAGAATTGCTCATTATGTAATACTTTAATTCTACTCTTTTGTATTAGCTACATTA
 CCTTGTGAAGCAGTACACATTTGTCCTTTTAAAGACGTGAAAGCTCTGAAATTAATTTTAG
 AGGATATTAATTGTGATTTTATGTTTGTAACTACAACCTTTCAAAGCATTCACTGATGGT
 CTGCTAGGTTTCAAGGCTGTAGTTTACAAAAAGCAATATTGCAAGTGAATATGTGATTCTTTAA
 GGCTGCAATTAAGCAGCTCAGTTCCTGTTTCAATAAGAGTCAATCCACATTTACAAGATG
 CATTTTTTCTTTTTGTATAAAAAAGCAATAATATTGCGCTCAGATTATTTCTCAAAATA
 TAACACATATCTAGATTTTCTGCTTGCATGATATTCAGGTTTCAGGAATGAGCCTTGTAAAT
 ATAAGTGGCTGTGAGCTCTGCTTCTCTTCTGTAAGTTGAGTGGGTGAGCTTCTATAC
 AATAATATTTTCTCTTGTCTCCAACATAATAAATGTTTTGTAAATCTTACAATTTGA
 AAGTAAAAATAAACAGAGTGATCAAGTTAAACCATACACTATCTCAAGTAACGAGGAGC
 TATTGGACTGTAAAAATCTCTCTGCACTGACAAATGGGGTTTGAAGAATTTGCCCCACACT
 AACTCAGTTCTTGTGATGAGAGACAAATTAATAACAGTATAGTAAATATACCATATGATTTC
 TTAGTTGTAGCTAAATTTAGATCCACCGTGGGAAATCAITTCCTTTAAATGACAGACA
 GTCCACTCAAAGGATTGCTAGCAATACAGCATCTTTTCTTTCACTAGTCCAAGCCAAAAA
 TTTTAAGATGATTTGTGAGAAAGGGCAAAAGTCTATCACCTAATATTACAAGAGTTGGTA
 AGCGCTCATCATTTATTTTATTTTGTGGCAGGTATATGACAGTGCAGCTGGAGGGTATGGGA
 TATGGATATGGACGTTCCAGAGACTATAATGGCAGAAACAGGGGTGGTTATGACCGCTACTC
 AGGAGGAATTAACAGACAAATTATGACAACTGAAATGAGACATGCACATATAGATACA
 CAAGGAATAATTTCTGATCCAGGATCGTCTTCCAAATGGCTGTATTTATAAAGGTTTTTGG
 AGCTGCAGTGAAGCATCTTATTTATAGTATATCAACCTTTTGTTTTAAATGAGCTGCCA
 AGGTAGCTGAAGACCTTTTATGACAGTCCATCTTTTTTTTTTAAATTTCTGCGCTATTTAA
 AGACAAATATGAGGAGCTTTGTCAAAAAAATAAAAAAATAAAAAA

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MLLLVQGACCSNQWLA AVL LSLCLLPSCLPAGQSVDPFWAAVDNMVRKGD TAVLR CYLED
 GASKGAWLNRSSI IPAGGDKWSVDP RVS ISTLNKR DYSLQ TQNVDTDDGPYTC SVQTQHTP
 RTMQVHLTVQVPFKIYDISNDMTVNEGNTNVTLTCLATGKPEPSISWRHISPSAKPFENGQYL
 DIYGITRDQAGEYECSAENAVSFPDVRKVKVVFNPATITQEI KSGTVTPGRSGLIRCEGAGV
 PPAPAFWEYKGEKLLPFGQQGIIQIFNSTRILTVNTV TQEHFNGNYTCVAANKLGTTNASLPL
 NPPSTAOGYGTSGADVLFGSCWYLLVLTLSFSTSI FYFLKNAILLO

Important features of the protein:

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 326-345

N-glycosylation sites.

amino acids 71-75, 153-157, 273-277, 284-288, 292-296, 305-309

Casein kinase II phosphorylation site.

amino acids 147-151, 208-212, 224-228

Tyrosine kinase phosphorylation site.

amino acids 178-186

N-myristoylation sites.

amino acids 7-13, 63-70, 67-73, 151-157, 239-245, 291-297,
302-308, 319-325

Myelin P0 protein:

amino acids 92-121

FIGURE 231

AGTGGTTCGATGGGAAGGATCTTTCTCCAAGTGGTTCCTCTTGAGGGGAGCATTCTCTGCTGG
CTCCAGGACTTTGGCCATCTATAAAGCTTGGCAATGGAGAAATAAGAAAATTCTCAAGGAGGA
CGAGCTCTTGAGTGAGACCCAACAGCTGCTTTTCACCAAATTGCAATGGAGCCTTTCGAAA
TCAATGTTCCAAAGCCCAAGAGGAGAAATGGGGTGAACTTCTCCCTAGCTGTGGTGGTCATC
TACCTGATCCTGCTCACCGCTGGCGCTGGGCTGCTGGTGGTCCAAAGTCTCTGAATCTGCAGGC
GCGGCTCCGGGTCTCGGAGATGTATTTCTCAATGACACTCTGGCGGTGAGGACAGCCCGT
CCTTCTCCTTGCTGCAGTCAGCACACCCTGGAGAACACCTGGCTCAGGGTGATCGAGGCTG
CAAGTCTGTCAGGCCCCAATCACCTGGGTCCGCGTCAGCCATGAGCACTTGCTGTCAGCGGGT
AGACAACCTCACTCAGAACCAGGGATGTTCAGAATCAAAGGTGAACAAGGCGCCCCAGGTC
TTCAAGGTCACAAGGGGGCCATGGGCATGCTGGTGCCCTTGGCCCCGCGGACCACTGCT
GAGAAGGGAGCCAAAGGGGCTATGGGACGAGATGGAGCAACAGGCCCCCTCGGGACCCCAAGG
CCCACCGGGAGTCAAGGGAGAGGCGGGCTCCAAGGACCCAGGGTGCTCAGGGAAGCAAG
GAGCCACTGGCACCCAGGACCCCAAGGAGAGAAGGGCAGCAAAGGCGATGGGGTCTCATTT
GGCCCCAAAAGGGGAACTGGAACATAAGGGAGAGAAAGGAGACCTGGGTCTCCAGGAAGCAA
AGGGGACAGGGGCATGAAAGGAGATGCAGGGGTCTATGGGGCTCTCTGGAGCCCAGGGGAGTA
AAGGTGACTTCGGGAGGCCAGGCCCCACAGGTTTGGCTGGTTTCTCTGGAGCTAAAGGAGAT
CAAGGACAACCTGGACTGCAGGGTGTTCCGGGCCCTCTGGTGCGATGGGACACCCAGGTGC
CAAGGGTGAGCTTGGCAGTGCTGGCTCCCTTGGCGAGCAGGACTTCCAGGGAGCCCCGGGA
GTCAGGAGGCCACAGGCCTGAAAGGAAGCAAAGGGGACACAGGACTTCAAGGACAGCAAGGA
AGAAAAGGAGAATCAGGAGTTCAGGCCCTGCAAGGTGTGAAGGGAGAACAGGGGAGCCAGG
GCTGGCAGGTCCCAGGGAGCCCTTGACAAAGCTGGCCAGAAGGGAGACCAGGGAGTGAAAG
GATCTTCTGGGGAGCAAGGAGTAAAGGGAGAAAAGGTGAAAGAGGTGAAAACCTCAGTGTCC
GTCAGGATTGTGCGCAGTAGTAACCGAGGCCGGGCTGAAGTTTACTACAGTGGTACCTGGGG
GACAATTTGCGATGACGAGTGGCAAAATTCTGATGCCATTGTCTTCTGCCCGATGCTGGGTT
ACTCCAAAGGAAGGGCCCTGTACAAAGTGGGAGCTGGCACTGGGCAGATCTGGCTGGATAAT
GTTCACTGTGCGGGGACGAGAGTAGCTACCTGTGGAGCTGCACCAAGAAATAGCTGGGGCCATCA
TGACTGCAGCCACGAGGAGGACGACGGCGTGGAGTGCAGCGTCTTGACCCCGGAACCTTTTCA
CTTCTCTGCTCCCGAGGTGTCTCGGGCTCATATGTGGGAAGGCGAGAGGATCTCTGAGGAGT
TCCCTGGGGACAACCTGAGCAGCCTCTGGAGAGGGGCCATTAATAAGGCTCAACATCATTGA

FIGURE 232

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886

><subunit 1 of 1, 520 aa, 1 stop

><MW: 52658, pI: 9.16, NX(S/T): 3

MRNKKILKEDELLSETQQAAPHQIAMEPFEINVPKPKRRNGVNFSLAVVVIYLIILLTAGAGL
LVVQVLNLQARLRVLEMYFLNDTLAAEDSPSPSLLQSAHPGEHLAQGASRLQVLQAQLTWVR
VSHEHLLQRVDNFTQNPGMFRIKGEQGAPGLQGHKGAMMPGAPGPPGPPAEKGAKGAMGRD
GATGPPSGPPQPGVVKGEAGLQGPQGAPGKQGATGTPGPQGEKGSKGDGGLIGPKGETGTKGE
KGDGLGLPGSKGDRGMKGDAVGMPPGAQGSKGDFGRPGPPGLAGFPGAAGDQGGQGLQGVPG
PPGAVGHLPKAGKEPGSAGSPGRAGLPGSPGSPGATGLKGSKGDGTGLQGQQGRKGESGVPGPA
GVKGEQGSPLAGPKGAPGQAGQKGDQGVKGSSGEQGVKGEKGERGENSVSVRIVGSSNRGR
AEVYYSGTWGTICDDEWQNSDAIVFCRMLGYSKGRALYKVGAGTGQIWLDDNVQCRGTESTLW
SCTKNSWGHDCSHEEDAGVECSV

Transmembrane domain:

amino acids 47-66 (type II)

N-glycosylation sites.

amino acids 43-47, 83-87, 136-140

Tyrosine kinase phosphorylation site.

amino acids 432-440

N-myristoylation sites.

amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,
400-406, 441-447, 475-481, 490-496, 515-521

Amidation site.

amino acids 360-364

Leucine zipper pattern.

amino acids 56-78

Speract receptor repeat

amino acids 422-471, 488-519

Clq domain proteins.

amino acids 151-184, 301-334, 316-349

003101-4998/663

FIGURE 233

CCCACGCGTCCGAAGGCAGACAAAGGTTCAATTTGTAAAGAAGCTCCTTCCAGCACCTCCTCT
CTTCTCCTTTTGCCCAAACCTACCCAGTGAGTGTGAGCATTTAAGAAGCATCCTCTGCCAAG
ACCAAAAGGAAAGAAGAAAAAGGGCCAAAAGCCAAAATGAAACTGATGGTACTTGTTTTCAC
CATTGGGGTAACTTTGCTGCTAGGAGTTCAAGCCATGCCTGCAAATCGCCTCTCTTGCTACA
GAAAGATACTAAAAGATCACAACCTGTCAACCTTCCGGAAGGAGTAGCTGACCTGACACAG
ATTGATGTCAATGTCCAGGATCATTTCTGGGATGGGAAGGGATGTGAGATGATCTGTTACTG
CAACTTCAGCGAATTGCTCTGCTGCCCAAAGACGTTTTCTTTGGACCAAAGATCTCTTTCG
TGATTCTTGCAAACATCAATGAGAATCTTCATGTATTCTGGAGAACACCATTCTGATTTTC
CCACAACTGCACTACATCAGTATAACTGCATTTCTAGTTTCTATATAGTGCAATAGAGCAT
AGATTCTATAAATCTTACTTGTCTAAGACAAGTAAATCTGTGTTAAACAAGTAGTAATAAA
AGTTAATTCAATCTAAAAAAAAAAAAA

09978564.101501

FIGURE 234

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52758
<subunit 1 of 1, 98 aa, 1 stop
<MW: 11081, pI: 6.68, NX(S/T): 1
MKLMVLVFTIGLTLLLGVSQAMPANRLSCYRKILKDHNCHNLPEGVADLTQIDVNVQDHFWDG
KGCEMICYCNFSELLCCPKDVFPGPKISFVIPCNNQ

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-76

Tyrosine kinase phosphorylation site.

amino acids 63-71

FIGURE 235

CCCACGCGTCCGCGGACGCGTGGGCTGGACCCAGGTCTGGAGCGAATTCAGCCTGCAGGG
 CTGATAAGCGAGGCATTAGTGAGATTGAGAGAGACTTTACCCGCGCGTGGTGGTGGAGGGC
 GCGCAGTAGACGAGCAGCAGCAGCGCGGGTCCCGGAGGCCGGCTCTGCTCGCGCCGAGATG
 TGGAAATCTCCTTCACGAAACCGACTCGGCTGTGGCCACCGCGCGCCGCCGCTGGCTGTG
 CGCTGGGGCGCTGGTGCTGGCGGGTGGCTTCTTTCTCCTCGGCTTCTCTTCGGGTGGTTTA
 TAAATCCTCCAATGAAGCTACTAACATTACTCCAAAGCATAATATGAAAGCATTTTGGAT
 GAATTGAAAGCTGAGAACATCAAGAAGTTCTTACATAATTTTACACAGATACCACATTTAGC
 AGGAACAGAACAAACTTTCAGCTTGCAAAGCAAATTCATCCAGTGGAAAGAAATTGGCC
 TGGATTCTGTTGAGCTAGCTCATTATGATGTCCTGTTGTCTTACCCAAATAAGACTCATCCC
 AACTACATCTCAATAATTAAATGAAGATGGAATGAGATTTTCAACACATCATTATTTGAACC
 ACCTCCTCCAGGATATGAAAATGTTTCGGATATTGTACCACCTTTTCAGTGCTTTCTCTCCTC
 AAGGAATGCCAGAGGGCGATCTAGTGATGTTAACTATGCACGAACCTGAAGACTTCTTTAA
 TTGGAACGGGACATGAAAATCAATTGCTCTGGGAAAATTTGTAATTGCCAGATATGGGAAAGT
 TTTTCAGAGGAAATAAGGTTAAATAATGCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACT
 CCGACCTGCTGACTACTTTGCTCCTGGGGTGAAGTCCATCCAGACGGTTGGAATCTTCTCT
 GGAGTGGTGTCCAGCGTGGGAAATAATCTAAATCTGAATGGTGAGGACCTCTCACAC
 AGGTTACCCAGCAAATGAATATGCTTATAGGCGTGAATTCAGAGGCTGTTGGTCTTCCAA
 GTATTCTGTTTCATCCAATTTGGATACATGATGCACAGAAGCTCTAGAAAAAATGGGTGGC
 TCAGCACCACCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAAATGTTGGACCTGG
 CTTTACTGGAACCTTTTCTACAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGA
 CGAGAAATTACAATGTGATAGGTAATCTCAGAGGAGCAGTGGAAACCAGACAGATATGTCATT
 CTGGGAGGTACCCGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAGAGTGGAGCAGCTGT
 TGTTTCATGAAATTGTGAGGAGCTTTGGAACACTGAAAAGGAAGGTTGGAGACCTAGAAGAA
 CAATTTTGTTTGCAAGCTGGGATGCAGAAGAATTGGTCTTCTGTGTTCTACTAGTGGGCA
 GAGGAGAATTCAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCTAT
 AGAAGGAAACTACACTCTGAGAGTTGATTGTACACCGCTGATGTACAGCTTGGTACACAACC
 TAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTCTTTATGAAAGTTGG
 ACTAAAAAAGTCTTCTCCAGAGTTGAGTGGCATGCCAGGATAAGCAAATTTGGGATCTGG
 AAATGATTTTGAAGTGTCTTCTTCAACGCAATGGAATGCTTCAGGCAGAGCACGGTATACTA
 AAAATTTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATCAAGTGTCATGAAACATAT
 GAGTTGGTGGAAAAGTTTATGATCCAATGTTTAAATATCACTCTACTGTGGCCAGGTTTCG
 AGGAGGATGGTGTTTGAGCTAGCCAATTCATAGTGCTCCCTTTTGATTGTGAGATTATG
 CTGTAGTTTAAAGAAAGTATGCTGACAAAATCTACAGTATTTCTATGAAACATCCACAGGAA
 ATGAAGACATACAGTGTATCATTGATTCACTTTTTCTGCGAGTAAAGAATTTTACAGAAAT
 TGCTTCCAAGTTCACTGAGAGACTCCAGGACTTTGACAAAAGCAACCCAATAGTATTGAAGAA
 TGATGAATGATCACTCATGTTTCTGGAAGAGACATTTATTGATCACTTAGGTTTACCAGAC
 AGGCTCTTTTATAGGATGTCATCTATGCTCCAAGCAGCCACCAAGTATGCGAGGGAGTC
 ATTCCAGGAATTTATGATGCTCTGTTTGTATATTGAAAGCAAAGTGGACCTTCCAAGGCCCT
 GGGGAGAAGTGAAGAGACAGATTTATGTTGCAGCCTTACAGTGGCAGGCAGCTGCAGAGACT
 TTGAGTGAAGTAGCTTAAAGGATTTTATAGAGAATCCGATTTGAATTTGTGTGGTATGTCA
 CTGAGAAAGAAATCGTAATGGGTATATTGATAAAATTTAAAAATTTGGTATATTGAAATAAAGT
 TGAATATTATATATAA

09978554.101601

FIGURE 236

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA52756

><subunit 1 of 1, 750 aa, 1 stop

><MW: 84305, pI: 6.93, NX(S/T): 10

MWNLLHETDSAVATARRPRWLCAGALVLAGGFLLGLFLGWFIKSSNEATNITPKHNMKAPL
DELKAENIKKFLHNFTQIPHLAGTEQNFQLAKQIQSQWKEFGLDSELAHYDVLSSYPNKT
PNYISIIINEDGNEIFNTSLFEPPPPGYENVSDIVPPFSAFSPQGMPEGLVYVNYARTEDFF
KLERDMKINCSCGKIVARIYRGKVFGRGNKVKNQLAGAKGVILYSDPADYFAPGVKSYPDGWNL
PGGGVQRGNILNLNGAGDPLTPGYPANERYARRGIAEAVGLPSIPVHPIGYYDAQKLEKMG
GSAPPDSSWRGSLKVPYNVGPFTGNFSTQKVKMHIHSTNEVTIRIYNVIGTLRGAVEPDRYV
ILGGHRDSWVFGGIDPQSGAAVVHEIVRSFGLTKKEGWRPRRTILFASWDAEEFGLLGSTEW
AEENSRLQLBERGVAYINADSSIEGNYTLRVDCTPLMYSLVHNLTKEKLSPEDEGFEGKSLYES
WTKKSPSPSEFGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSGYPLYHSVYET
YELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRKYADKIYSISMKHPQ
EMKTYSVSFDLSFSAVKNFTEIASKFSERLQDFDKSNPIVLRMMNDQLMFLERAFIDPLGLP
DRPFYRHVIYAPSSHKNKYAGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAFTVQAAAE
TLSEVA

Signal sequence:

amino acids 1-40

N-glycosylation sites.

amino acids 76-80, 121-125, 140-144, 153-157, 195-199, 336-340,
459-463, 476-480, 638-642

Tyrosine kinase phosphorylation sites.

amino acids 363-372, 605-613, 606-613, 617-626

N-myristoylation sites.

amino acids 85-91, 168-174, 252-258, 256-262, 282-288, 335-341,
360-366, 427-433, 529-535, 707-713